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OM protein - protein search, using sw model

Run on: December 3, 2005, 13:27:13 ; Search time 146.743 Seconds
(without alignments)
304.667 Million cell updates/sec

Title: US-10-769-144-8

Perfect score: 557

Sequence: 1 DIQMTQSPSSLSASVGRVT.....CQQNSYPRTFGQGTKEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

- Published Applications_AA Main:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	557	100.0	107	3	US-09-851-614-2
2	557	100.0	107	4	US-10-035-637-2
3	557	100.0	107	5	US-10-769-144-8
4	557	100.0	107	5	US-10-903-191-8
5	557	100.0	233	5	US-10-769-144-6
6	557	100.0	233	5	US-10-903-191-6
7	557	100.0	411	5	US-10-769-144-12
8	557	100.0	411	5	US-10-903-191-12
9	538	96.6	107	3	US-09-948-939-13
10	538	96.6	107	6	US-11-040-846-13
11	538	96.6	108	4	US-10-408-901-20
12	538	96.6	214	4	US-10-408-901-44
13	537	96.4	107	5	US-10-891-658-88
14	535	96.1	107	4	US-10-703-714-4
15	535	96.1	107	4	US-10-703-714-8
16	535	96.1	107	4	US-10-703-714-16
17	535	96.1	236	5	US-10-858-186-20
18	531	95.3	107	5	US-10-815-449-6
19	531	95.3	107	6	US-11-009-731-91
20	531	95.3	107	6	US-11-102-403-13
21	530	95.2	107	4	US-10-221-529-4
22	529	95.0	107	5	US-10-815-449-2
23	529	95.0	107	5	US-10-815-449-4
24	529	95.0	108	3	US-09-920-262A-8
25	529	95.0	108	3	US-10-912-994-8
26	529	95.0	108	5	US-10-975-883-8
27	529	95.0	108	5	US-10-975-740A-8

28	529	95.0	108	5	US-10-975-708-8	Sequence 8, Appli
29	526	94.4	107	6	US-11-102-403-5	Sequence 5, Appli
30	526	94.4	107	6	US-11-102-403-7	Sequence 7, Appli
31	524	94.1	108	4	US-10-408-901-12	Sequence 12, Appli
32	524	94.1	214	4	US-10-408-901-36	Sequence 36, Appli
33	522	93.7	107	6	US-11-102-403-15	Sequence 15, Appli
34	521	93.5	128	4	US-10-389-221-12	Sequence 12, Appli
35	521	93.5	128	5	US-10-909-851-26	Sequence 26, Appli
36	519	93.2	107	4	US-10-338-366-12	Sequence 12, Appli
37	508	91.2	107	5	US-10-727-155-312	Sequence 312, App
38	508	91.2	129	5	US-10-910-901-20	Sequence 20, Appli
39	506	90.8	107	4	US-10-041-860-43	Sequence 43, Appli
40	506	90.8	107	4	US-10-041-860-218	Sequence 218, App
41	506	90.8	107	4	US-10-685-383-64	Sequence 64, Appli
42	505	90.7	127	4	US-10-395-894-25	Sequence 25, Appli
43	505	90.7	127	4	US-10-695-667-25	Sequence 25, Appli
44	505	90.7	127	5	US-10-976-352-25	Sequence 25, Appli
45	504	90.5	107	5	US-10-727-155-122	Sequence 122, App

ALIGNMENTS

RESULT 1

US-09-851-614-2
; Sequence 2, Application US/09851614
; Publication No. US20030167502A1
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Keler, Tibor
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
; FILE REFERENCE: MXI-166
; CURRENT APPLICATION NUMBER: US/09/851.614
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: USN 60/203.126
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: USN 60/230.739
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-851-614-2

Query Match	100.0%;	Score	557;	DB 3;	Length	107;
Best Local Similarity	100.0%;	Pred. No.	2.6e-42;			
Matches	107;	Conservative	0;	Mismatches	0;	Indels
						Gaps
						0;
Qy	1	DIQMTQSPSSLSASVGRVTITCRASQGISRWLA	YQKPKAPKSLIYAASSLSQGVPS	60		
Db	1	DIQMTQSPSSLSASVGRVTITCRASQGISRWLA	YQKPKAPKSLIYAASSLSQGVPS	60		
Qy	61	RFGSGSGTDTLTISGLQPEDFATYYCQYNSYPR	TFGQGTKEIK	107		
Db	61	RFGSGSGTDTLTISGLQPEDFATYYCQYNSYPR	TFGQGTKEIK	107		

RESULT 2

US-10-035-637-2
; Sequence 2, Application US/10035637
; Publication No. US20030031667A1
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Keler, Tibor
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
; FILE REFERENCE: MXI-166CP
; CURRENT APPLICATION NUMBER: US/10/035.637
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 09/851.614

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; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USN 60/203,126
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: USN 60/230,739
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-035-637-2

Query Match      100.0%; Score 557; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.6e-42;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDVRTTTCRASQGISRWLAQQKPEKAPKSLIYAASSLSQGVPS 60
Db 1 DIQWTQSPSSLSASVGDVRTTTCRASQGISRWLAQQKPEKAPKSLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDFTLTISGLQPEDFATYCCQYNSYPRTFGGTKVEIK 107
Db 61 RFGSGSGTDFTLTISGLQPEDFATYCCQYNSYPRTFGGTKVEIK 107

RESULT 3
US-10-769-144-8
; Sequence 8, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10769,144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-8

Query Match      100.0%; Score 557; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.6e-42;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDVRTTTCRASQGISRWLAQQKPEKAPKSLIYAASSLSQGVPS 60
Db 1 DIQWTQSPSSLSASVGDVRTTTCRASQGISRWLAQQKPEKAPKSLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDFTLTISGLQPEDFATYCCQYNSYPRTFGGTKVEIK 107
Db 61 RFGSGSGTDFTLTISGLQPEDFATYCCQYNSYPRTFGGTKVEIK 107

RESULT 4
US-10-903-191-8
; Sequence 8, Application US/10903191
; Publication No. US20050180983A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
```

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; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301CP
; CURRENT APPLICATION NUMBER: US/10/903,191
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/769144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-903-191-8

Query Match      100.0%; Score 557; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.6e-42;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDVRTTTCRASQGISRWLAQQKPEKAPKSLIYAASSLSQGVPS 60
Db 1 DIQWTQSPSSLSASVGDVRTTTCRASQGISRWLAQQKPEKAPKSLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDFTLTISGLQPEDFATYCCQYNSYPRTFGGTKVEIK 107
Db 61 RFGSGSGTDFTLTISGLQPEDFATYCCQYNSYPRTFGGTKVEIK 107

RESULT 5
US-10-769-144-6
; Sequence 6, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-6

Query Match      100.0%; Score 557; DB 5; Length 233;
Best Local Similarity 100.0%; Pred. No. 5.6e-42;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDVRTTTCRASQGISRWLAQQKPEKAPKSLIYAASSLSQGVPS 60
Db 20 DIQWTQSPSSLSASVGDVRTTTCRASQGISRWLAQQKPEKAPKSLIYAASSLSQGVPS 79
Qy 61 RFGSGSGTDFTLTISGLQPEDFATYCCQYNSYPRTFGGTKVEIK 107
Db 80 RFGSGSGTDFTLTISGLQPEDFATYCCQYNSYPRTFGGTKVEIK 126

RESULT 6
US-10-903-191-6
; Sequence 6, Application US/10903191
; Publication No. US20050180983A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
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; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301CP
; CURRENT APPLICATION NUMBER: US/10/903,191
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/769144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-903-191-6

Query Match      100.0%; Score 557; DB 5; Length 233;
Best Local Similarity 100.0%; Pred. No. 5.6e-42;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60
Db 20 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 79

Qy 61 RFGSGSGTDFLTITISGLQPEDFATYYCQYNSYPRTFGGTKVEIK 107
Db 80 RFGSGSGTDFLTITISGLQPEDFATYYCQYNSYPRTFGGTKVEIK 126

RESULT 7
US-10-769-144-12
; Sequence 12, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-769-144-12

Query Match      100.0%; Score 557; DB 5; Length 411;
Best Local Similarity 100.0%; Pred. No. 1e-41;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60
Db 20 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 79

Qy 61 RFGSGSGTDFLTITISGLQPEDFATYYCQYNSYPRTFGGTKVEIK 107
Db 80 RFGSGSGTDFLTITISGLQPEDFATYYCQYNSYPRTFGGTKVEIK 126

RESULT 8
US-10-903-191-12
; Sequence 12, Application US/10903191
; Publication No. US20050180983A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301CP
; CURRENT APPLICATION NUMBER: US/10/903,191
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/769144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-903-191-12

Query Match      96.6%; Score 538; DB 3; Length 107;
Best Local Similarity 97.2%; Pred. No. 1.3e-40;
Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDFLTITISGLQPEDFATYYCQYNSYPRTFGGTKVEIK 107
Db 61 RFGSGSGTDFLTITISGLQPEDFATYYCQYNSYPRTFGGTKVEIK 126

; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301CP
; CURRENT APPLICATION NUMBER: US/10/903,191
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/769144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-903-191-12

Query Match      100.0%; Score 557; DB 5; Length 411;
Best Local Similarity 100.0%; Pred. No. 1e-41;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60
Db 20 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 79

Qy 61 RFGSGSGTDFLTITISGLQPEDFATYYCQYNSYPRTFGGTKVEIK 107
Db 80 RFGSGSGTDFLTITISGLQPEDFATYYCQYNSYPRTFGGTKVEIK 126

RESULT 9
US-09-948-939-13
; Sequence 13, Application US/09948939
; Publication No. US20020086014A1
; GENERAL INFORMATION:
; APPLICANT: Korman, Alan J.
; APPLICANT: Halk, Edward L.
; APPLICANT: Lonberg, Nils
; APPLICANT: Medarex, Inc.
; TITLE OF INVENTION: Human CTLA-4 Antibodies and Their Uses
; FILE REFERENCE: 014643-010520US
; CURRENT APPLICATION NUMBER: US/09/948,939
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/150,452
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: 09/644,668
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 13
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: light chain variable region predicted sequence for
; OTHER INFORMATION: 1E2 from Vκ L-15
; US-09-948-939-13

Query Match      96.6%; Score 538; DB 3; Length 107;
Best Local Similarity 97.2%; Pred. No. 1.3e-40;
Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDFLTITISGLQPEDFATYYCQYNSYPRTFGGTKVEIK 107
Db 61 RFGSGSGTDFLTITISGLQPEDFATYYCQYNSYPRTFGGTKVEIK 107
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Db 61 RFGSGSGTDFTLTISLQPEDFATYYCQYNSYPRTFGQGTKEIK 107

RESULT 10

US-10-846-13
; Sequence 13, Application US/11040846
; Publication No. US20050201994A1
; GENERAL INFORMATION:
; APPLICANT: Korman, Alan J.
; APPLICANT: Halk, Edward L.
; APPLICANT: Loberg, Nils
; APPLICANT: Medarex, Inc.
; TITLE OF INVENTION: Human CTLA-4 Antibodies and Their Uses
; FILE REFERENCE: 014643-010520US
; CURRENT APPLICATION NUMBER: US/11/040,846
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US/09/948,939
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/150,452
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: 09/644,668
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: light chain variable region predicted sequence for
; OTHER INFORMATION: 1B2 from V κ L-15
US-10-846-13

Query Match 96.6%; Score 538; DB 6; Length 107;
Best Local Similarity 97.2%; Pred. No. 1.3e-40;
Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 1 DIQWTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDFTLTISLQPEDFATYYCQYNSYPRTFGQGTKEIK 107
Db 61 RFGSGSGTDFTLTISLQPEDFATYYCQYNSYPRTFGQGTKEIK 107

RESULT 11

US-10-408-901-20
; Sequence 20, Application US/10408901
; Publication No. US20040023313A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Huang, Haichun
; APPLICANT: Elliot, Robin
; APPLICANT: Sullivan, John
; APPLICANT: Medlock, Eugene
; APPLICANT: Martin, Francis
; TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
; FILE REFERENCE: MBHB 01-1145-A
; CURRENT APPLICATION NUMBER: US/10/408,901
; CURRENT FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-901-20

Query Match 96.6%; Score 538; DB 4; Length 108;
Best Local Similarity 97.2%; Pred. No. 1.3e-40;
Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 1 DIQWTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDFTLTISLQPEDFATYYCQYNSYPRTFGQGTKEIK 107
Db 61 RFGSGSGTDFTLTISLQPEDFATYYCQYNSYPRTFGQGTKEIK 107

RESULT 12

US-10-408-901-44
; Sequence 44, Application US/10408901
; Publication No. US20040023313A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Huang, Haichun
; APPLICANT: Elliot, Robin
; APPLICANT: Sullivan, John
; APPLICANT: Medlock, Eugene
; APPLICANT: Martin, Francis
; TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
; FILE REFERENCE: MBHB 01-1145-A
; CURRENT APPLICATION NUMBER: US/10/408,901
; CURRENT FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-901-44

Query Match 96.6%; Score 538; DB 4; Length 214;
Best Local Similarity 97.2%; Pred. No. 2.6e-40;
Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 1 DIQWTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDFTLTISLQPEDFATYYCQYNSYPRTFGQGTKEIK 107
Db 61 RFGSGSGTDFTLTISLQPEDFATYYCQYNSYPRTFGQGTKEIK 107

RESULT 13

US-10-891-658-88
; Sequence 88, Application US/10891658
; Publication No. US20050074821A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth, Wild
; APPLICANT: Treanor, James
; APPLICANT: Huang, Haichun
; APPLICANT: Inoue, Heather
; APPLICANT: Zhang, Tie J.
; APPLICANT: Martin, Frank
; TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway
; FILE REFERENCE: 02-1240
; CURRENT APPLICATION NUMBER: US/10/891,658
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/487,431
; PRIOR FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 88
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapien
US-10-891-658-88


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Qy 1 DIOMTQSSSLGASGVDRTTITCRASQGISRLWAWYQOKPEKAPKSLIYAASSLQSGVPS 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 DIOMTQSSSLGASGVDRTTITCRASQGISRLWAWYQOKPEKAPKSLIYAASSLQSGVPS 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 61 RFSGSGSGTDFTLTISGLQPEDFATYYCOQYNSYPRTFGQGTKEIK 107
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 RFSGSGSGTDFTLTISGLQPEDFATYYCOQYNSYPRTFGQGTKEIK 107
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Job time : 147.743 secs

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Search completed: December 3, 2005, 14:17:34
Job time : 147.743 secs

[illegible]

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RESULT 15
US-10-703-714-8
; Sequence 8, Application US/10703714
; Publication No. US20040170630A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Haichun
; APPLICANT: Holmes, Steven
; APPLICANT: Mason, Sean
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HEPARANASE
; FILE REFERENCE: MXI-294
; CURRENT APPLICATION NUMBER: US/10/703,714
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 60/424803
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-703-714-8

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Query Match      96.1%; Score 535; DB 4; Length 107;
Best Local Similarity 96.3%; Pred. No. 2.4e-40;
Matches 103; Conservative 1; Mismatches 3; Indels 0; Gaps 0
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 13:48:29 ; Search time 6.11429 Seconds
(without alignments)
83.796 Million cell updates/sec

Title: US-10-769-144-8

Perfect score: 557

Sequence: 1 DIQWTSQSSLSASVGRVT.....CQQNSYPRTFGQTKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /cgn2_6/ptodata/1/pubpaa/US09 NEW PUB.pap.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pap.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pap.*
- 4: /cgn2_6/ptodata/1/pubpaa/US08 NEW PUB.pap.*
- 5: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pap.*
- 6: /cgn2_6/ptodata/1/pubpaa/US10 NEW PUB.pap.*
- 7: /cgn2_6/ptodata/1/pubpaa/US11 NEW PUB.pap.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60 NEW PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	495	88.9	244	7	US-11-054-515-1881
2	486	87.3	236	7	US-11-144-248-52
3	484	86.9	95	7	US-11-084-554-126
4	484	86.9	107	7	US-11-084-554-1
5	484	86.9	236	7	US-11-144-248-48
6	483	86.7	244	7	US-11-054-515-82
7	483	86.7	244	7	US-11-054-515-261
8	479	86.0	95	7	US-11-054-669-62
9	479	86.0	113	7	US-11-096-074-53
10	479	86.0	244	7	US-11-054-515-164
11	478	85.8	244	7	US-11-054-515-280
12	477	85.6	239	7	US-11-054-515-1882
13	477	85.6	239	7	US-11-054-515-1922
14	477	85.6	241	7	US-11-054-515-1889
15	477	85.6	241	7	US-11-054-515-1901
16	477	85.6	243	7	US-11-054-515-1883
17	477	85.6	243	7	US-11-054-515-1935
18	477	85.6	243	7	US-11-054-515-1945
19	477	85.6	243	7	US-11-054-515-2063
20	477	85.6	245	7	US-11-054-515-1900
21	477	85.6	245	7	US-11-054-515-1902
22	477	85.6	246	7	US-11-054-515-1920
23	477	85.6	246	7	US-11-054-515-2062
24	477	85.6	247	7	US-11-054-515-969
25	477	85.6	247	7	US-11-054-515-1177

ALIGNMENTS

RESULT 1

US-11-054-515-1881
; Sequence 1881, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1881
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-054-515-1881
Query Match 88.9%; Score 495; DB 7; Length 244;
Best Local Similarity 90.7%; Pred. NO. 1.7e-32;
Matches 97; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
QY 1 DIQWTSQSSLSASVGRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 137 DIQWTSQSSLSASVGRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 196
QY 61 RFGSGSGTDFLTITISGLQPEDFATYYCQYNSYPRTFGQTKVEIK 107
|||||

Sequence 1700, Ap
Sequence 1771, Ap
Sequence 1778, Ap
Sequence 918, App
Sequence 926, App
Sequence 1188, Ap
Sequence 932, App
Sequence 922, App
Sequence 1320, Ap
Sequence 1603, Ap
Sequence 1943, Ap
Sequence 2064, Ap
Sequence 3242, Ap
Sequence 1008, Ap
Sequence 1887, Ap
Sequence 51, Appl
Sequence 1806, Ap
Sequence 2003, Ap
Sequence 2005, Ap

Db 197 RFSGSGTGDTTLTISLQPEDFATYYCQANSFPLTFGGTKVEIK 243

RESULT 2

US-11-144-248-52

; Sequence 52, Application US/11144248

; Publication No. US20050244408A1

; GENERAL INFORMATION:

; APPLICANT: Cohen, Bruce D.

; APPLICANT: Beebe, Jean

; APPLICANT: Miller, Penelope E.

; APPLICANT: Moyer, James D.

; APPLICANT: Corvalan, Jose R.

; APPLICANT: Gallo, Michael

; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR

; FILE REFERENCE: ABX-PF2

; CURRENT APPLICATION NUMBER: US/11/144,248

; CURRENT FILING DATE: 2005-06-02

; PRIOR APPLICATION NUMBER: US/10/038,591

; PRIOR FILING DATE: 2002-01-04

; PRIOR APPLICATION NUMBER: 60/259,927

; PRIOR FILING DATE: 2001-01-05

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 52

; LENGTH: 236

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-144-248-52

Query Match 87.3%; Score 486; DB 7; Length 236;

Best Local Similarity 89.7%; Pred. No. 8.2e-32; Length 236;

Matches 96; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAHYQQKPKAPKSLIYAASSLSQGVPS 60

Db 23 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAHYQQKPKAPKSLIYAASSLSQGVPS 82

Qy 61 RFSGSGTGDTTLTISGLQPEDFATYYCQVNSYPRTFGGTKVEIK 107

Db 83 RFSGSGTGDTTLTISGLQPEDFATYYCLOHNSYPTWTFGGTKVEIK 129

RESULT 3

US-11-084-554-126

; Sequence 126, Application US/11084554

; Publication No. US20050260679A1

; GENERAL INFORMATION:

; APPLICANT: Kellermann, Sirid-Ai

; APPLICANT: Green, Larry L.

; APPLICANT: Korver, Wouter

; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN

; FILE REFERENCE: ABGENIX.100A

; CURRENT APPLICATION NUMBER: US/11/084,554

; CURRENT FILING DATE: 2005-03-17

; PRIOR APPLICATION NUMBER: 60/554,372

; PRIOR FILING DATE: 2004-03-19

; PRIOR APPLICATION NUMBER: 60/574,661

; PRIOR FILING DATE: 2004-05-24

; NUMBER OF SEQ ID NOS: 266

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 126

; LENGTH: 95

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-084-554-126

Query Match 86.9%; Score 484; DB 7; Length 95;

Best Local Similarity 97.9%; Pred. No. 5.5e-32;

Matches 93; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAHYQQKPKAPKSLIYAASSLSQGVPS 60

Db 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAHYQQKPKAPKSLIYAASSLSQGVPS 60

Qy 61 RFSGSGTGDTTLTISGLQPEDFATYYCQVNSYPRTFGGTKVEIK 95

Db 61 RFSGSGTGDTTLTISGLQPEDFATYYCQVNSYPRTFGGTKVEIK 95

RESULT 4

US-11-084-554-1

; Sequence 1, Application US/11084554

; Publication No. US20050260679A1

; GENERAL INFORMATION:

; APPLICANT: Kellermann, Sirid-Ai

; APPLICANT: Green, Larry L.

; APPLICANT: Korver, Wouter

; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN

; FILE REFERENCE: ABGENIX.100A

; CURRENT APPLICATION NUMBER: US/11/084,554

; CURRENT FILING DATE: 2005-03-17

; PRIOR APPLICATION NUMBER: 60/554,372

; PRIOR FILING DATE: 2004-03-19

; PRIOR APPLICATION NUMBER: 60/574,661

; PRIOR FILING DATE: 2004-05-24

; NUMBER OF SEQ ID NOS: 266

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 107

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-084-554-1

Query Match 86.9%; Score 484; DB 7; Length 107;

Best Local Similarity 88.8%; Pred. No. 6e-32;

Matches 95; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAHYQQKPKAPKSLIYAASSLSQGVPS 60

Db 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAHYQQKPKAPKSLIYAASSLSQGVPS 60

Qy 61 RFSGSGTGDTTLTISGLQPEDFATYYCQVNSYPRTFGGTKVEIK 107

Db 61 RFSGSGTGDTTLTISGLQPEDFATYYCQVNSYPRTFGGTKVEIK 107

RESULT 5

US-11-144-248-48

; Sequence 48, Application US/11144248

; Publication No. US20050244408A1

; GENERAL INFORMATION:

; APPLICANT: Cohen, Bruce D.

; APPLICANT: Beebe, Jean

; APPLICANT: Miller, Penelope E.

; APPLICANT: Moyer, James D.

; APPLICANT: Corvalan, Jose R.

; APPLICANT: Gallo, Michael

; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR

; FILE REFERENCE: ABX-PF2

; CURRENT APPLICATION NUMBER: US/11/144,248

; CURRENT FILING DATE: 2005-06-02

; PRIOR APPLICATION NUMBER: US/10/038,591

; PRIOR FILING DATE: 2002-01-04

; PRIOR APPLICATION NUMBER: 60/259,927

; PRIOR FILING DATE: 2001-01-05

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 48

; LENGTH: 236

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-144-248-48

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; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 261
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-261

Query Match 86.7%; Score 483; DB 7; Length 244;
Best Local Similarity 87.9%; Pred. No. 1.4e-31;
Matches 94; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAWYQQKPEKAPKSLIYAASSLQSGVPS 60
Db 137 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAWYQQKPEKAPKSLIYAASSLQSGVPS 196
QY 61 RFSGSGSGTDFTLTISGLQPEDPATYVCQYNSYPRTFGQGTKEIK 107
Db 197 RFSGSGSGTDFTLTISGLQPEDVATYVCQKYNAPYAFGGQGTKEIK 243

RESULT 8
US-11-054-669-62
; Sequence 62, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 62
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-62

Query Match 86.0%; Score 479; DB 7; Length 95;
Best Local Similarity 96.8%; Pred. No. 1.3e-31;
Matches 92; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAWYQQKPEKAPKSLIYAASSLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRAGISSWLAWYQQKPEKAPKSLIYAASSLQSGVPS 60
QY 61 RFSGSGSGTDFTLTISGLQPEDPATYVCQYNSYP 95

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Db 61 RFGSGSGTDTLTISLQPEDFATYCCQYNSYP 95
|||||
Query Match 86.0%; Score 479; DB 7; Length 113;
Best Local Similarity 86.7%; Pred. No. 1.5e-31;
Matches 98; Conservative 2; Mismatches 7; Indels 6; Gaps 2;

RESULT 9
US-11-096-074-53
; Sequence 53, Application US/11096074
; Publication No. US2005026193A1
; GENERAL INFORMATION:
; APPLICANT: LIEBERBURG, IVAN
; TITLE OF INVENTION: STEROID SPARING AGENTS AND METHODS OF USING SAME
; FILE REFERENCE: 034008-112
; CURRENT APPLICATION NUMBER: US/11/096,074
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: 60/558,120
; PRIOR FILING DATE: 2004-04-01
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 3.3
; SEQ ID NO 53
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (31)..(32)
; OTHER INFORMATION: Variable amino acid
US-11-096-074-53

Query Match 86.0%; Score 479; DB 7; Length 113;
Best Local Similarity 86.7%; Pred. No. 1.5e-31;
Matches 98; Conservative 2; Mismatches 7; Indels 6; Gaps 2;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQ-----GISRLAWYQOKPEKAPKSLIIYAASLIQ 55
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSLVXXSISNYLAWYQOKPEKAPKSLIIYAASLS 60
Qy 56 SGVSRFSGSGTDTLTISLQPEDFATYCCQYNSYPR-TFGQGTKEIK 107
Db 61 SGVSRFSGSGTDTLTISLQPEDFATYCCQYNSLPWTFGQGTKEIK 113

RESULT 10
US-11-054-515-164
; Sequence 164, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 280
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-280

Query Match 85.8%; Score 478; DB 7; Length 244;
Best Local Similarity 86.9%; Pred. No. 3.5e-31;
Matches 93; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRLAWYQOKPEKAPKSLIIYAASLIQSGVPS 60
Db 137 DIQMTQSPSSLSASIGDRVTITCRASQIRNYLAWYQOKPEKAPKSLIIYAASLIQSGVPS 196
Qy 61 RFGSGSGTDTLTISLQPEDFATYCCQYNSYPRTFGQGTKEIK 107
Db 197 RFGSGSGTDTLTISLQPEDVAAYYCKYNSAPYAFGQGTKEIK 243

RESULT 12
US-11-054-515-1882
; Sequence 1882, Application US/11054515
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```
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1882
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1882

Query Match      85.6%; Score 477; DB 7; Length 239;
Best Local Similarity 84.1%; Pred. No. 4.1e-31;
Matches 90; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 132 DIQMTQSPSTLSASIGDRVTITCRASEGIYHWLAWYQOKPGKAPKLLIYKASSLSGAPS 191
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 RFSGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFGGTKVEIK 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 192 RFSGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFGGTKVEIK 238
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 13
US-11-054-515-1889
; Sequence 1889, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1889
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1889

Query Match      85.6%; Score 477; DB 7; Length 241;
Best Local Similarity 84.1%; Pred. No. 4.1e-31;
Matches 90; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
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Db 134 DIQMTQSPSTLSASIGDRVTITCRASEGIYHWLAWYQOKPGKAPKLLIYKASSLSGAPS 193
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 RFSGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFGGTKVEIK 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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Mon Dec 5 12:41:11 2005

Db 194 RFGSGSGTDTLTITISSLPDDPATYCCQYSNYPLTFGGTKLEIK 240

RESULT 15

US-11-054-515-1901
; Sequence 1901, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
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; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1901
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1901

Query Match 85.6%; Score 477; DB 7; Length 241;
Best Local Similarity 84.1%; Pred. No. 4.1e-31;
Matches 90; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAHYQOKPEKAPKSLIYAASSLSQSGVPS 60
Db 134 DIQMTQSPSTLSASIGDRVTITCRASEGIYHMLAWYQOKPGKAPKLLIYKASSLSAGAPS 193
Qy 61 RFGSGSGTDTLTITISGLQPDPATYCCQYSNYPLTFGGTKVEIK 107
Db 194 RFGSGSGTDTLTITISSLPDDPATYCCQYSNYPLTFGGTKLEIK 240

Search completed: December 3, 2005, 14:17:54
Job time : 6.11429 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2005, 14:11:48 ; Search time 188.669 Seconds
(without alignments)
400.126 Million cell updates/sec

Title: US-10-769-144-8
Perfect score: 557
Sequence: 1 DIQMTQSPSSLSASVGRVT.....CQQNSYPRTFGQTKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	508	91.2	236	2	Q6GMX9 HUMAN
2	494	88.7	108	2	Q9UL70 HUMAN
3	494	88.7	236	2	Q6GMX8 HUMAN
4	492	88.3	236	2	Q502W4 HUMAN
5	481	86.4	236	2	Q723Y4 HUMAN
6	479	86.0	117	1	KV11 HUMAN
7	477	85.6	244	2	Q652C8 HUMAN
8	476	85.5	108	1	KV1G HUMAN
9	474	85.1	108	1	KV1V HUMAN
10	474	85.1	240	2	Q652C9 HUMAN
11	472	84.7	236	2	Q6GMW1 HUMAN
12	471	84.6	236	2	Q6PIH7 HUMAN
13	468	84.0	108	1	KV1F HUMAN
14	467	83.8	108	1	KV1L HUMAN
15	465	83.5	108	1	KV1R HUMAN
16	461	82.8	108	2	Q9UL77 HUMAN
17	460	82.6	108	2	Q9UL79 HUMAN
18	460	82.6	236	2	Q6PIH4 HUMAN
19	459	82.4	108	1	KV1H HUMAN
20	457	82.1	107	1	KV1D HUMAN
21	456	81.9	108	1	KV1A HUMAN
22	456	81.9	236	2	Q6P1T5 HUMAN
23	455	81.8	107	2	Q96SA9 HUMAN
24	453	81.3	108	1	KV1S HUMAN
25	448	80.4	234	2	Q72473 HUMAN
26	447	80.3	108	1	KV1M HUMAN
27	446	80.1	129	1	KV1W HUMAN
28	444	79.8	107	2	Q9UL81 HUMAN
29	443	79.5	108	1	KV1E HUMAN
30	443	79.5	236	2	Q6GMX0 HUMAN
31	441	79.2	108	1	KV1O HUMAN

32	440	79.0	108	1	KV1B HUMAN	P01594 homo sapien
33	439	78.8	117	1	KV1J HUMAN	P01602 homo sapien
34	438	78.6	108	1	KV1K HUMAN	P01603 homo sapien
35	435	78.1	108	1	KV1Y HUMAN	P80362 homo sapien
36	434	77.9	234	2	Q5EPF6 HUMAN	Q5efes6 homo sapien
37	433	77.7	108	1	KV1P HUMAN	P01608 homo sapien
38	429	77.0	108	1	KV1N HUMAN	P01606 homo sapien
39	428	76.8	108	1	KV1Q HUMAN	P01609 homo sapien
40	422	75.8	108	1	KV1C HUMAN	P01595 homo sapien
41	418	75.0	189	2	Q569T7 HUMAN	Q569t7 homo sapien
42	417	74.9	129	1	KV1X HUMAN	P04432 homo sapien
43	409	73.4	112	1	KV1U HUMAN	P01613 homo sapien
44	407	73.1	108	1	KV5J MOUSE	P01643 mus musculu
45	402	72.2	116	2	Q96PF6 HUMAN	Q96pf6 homo sapien

ALIGNMENTS

RESULT 1

Q6GMX9_HUMAN PRELIMINARY; PRT; 236 AA.

AC Q6GMX9; 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE IGKC protein.

GN Name=IGKC;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

XP [1]

NP NUCLEOTIDE SEQUENCE.

RP TISSUE=Primary B-Cells;

RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Smallos D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RL [2]

RN NUCLEOTIDE SEQUENCE.

RP	TISSUE=Primary B-Cells;
RC	NIH MGC Project;
RG	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL	EMBL; BC073763; AAH73763.1; -, mRNA.
DR	SMR; Q6GMX9; 23-236.
DR	Ensembl; ENSG00000163245; Homo sapiens.
DR	InterPro; IPR003599; IG.
DR	InterPro; IPR007110; IG-like.
DR	InterPro; IPR003597; IG cl.
DR	InterPro; IPR003006; IG_MHC.
DR	InterPro; IPR003596; IG_V.
DR	Pfam; PF07654; Cl-set; 1.
DR	SMART; SM00409; IG; 2.
DR	SMART; SM00407; IGcl; 1.

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DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG_LIKE; 2.  
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.  
SQ SEQUENCE 236 AA; 25924 MW; FDE2093DC560CF77 CRC64;  
  
Query Match 91.2%; Score 508; DB 2; Length 236;  
Best Local Similarity 90.7%; Pred. No. 2.1e-42;  
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
  
Qy 1 DIQWTSPPSSLSASVGRVTTTCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60  
Db 23 DIQWTSPPSSLSASVGRVTTTCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 82  
  
Qy 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNVSPRTFGGQTKVEIK 107  
Db 83 RFGSGSGTDFTLTISGLQPEDFATYYCQYNVSPRTFGGQTKVEIK 129  
  
RESULT 2  
Q9UL70 HUMAN  
ID Q9UL70_HUMAN PRELIMINARY; PRT; 108 AA.  
AC Q9UL70;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
Batterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RG NIH MGC Project;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073764; AAH73764.1; -, mRNA.  
DR SMR; Q6GMX8; 24-235.  
DR Ensembl; ENSG00000163245; Homo sapiens.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; IG_MHC.  
DR InterPro; IPR003596; IG_v.  
DR Pfam; PF07654; C1-set; 1.  
DR SMART; SM00409; IG1; 1.  
DR SMART; SM00406; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG_LIKE; 2.  
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.  
SQ SEQUENCE 236 AA; 25707 MW; 4FCBE14B6559EFC9 CRC64;  
  
Query Match 88.7%; Score 494; DB 2; Length 236;  
Best Local Similarity 89.7%; Pred. No. 5.2e-41;  
Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;  
  
Qy 1 DIQWTSPPSSLSASVGRVTTTCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60  
Db 23 DIQWTSPPSSLSASVGRVTTTCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 82  
  
Qy 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNVSPRTFGGQTKVEIK 107  
Db 83 RFGSGSGTDFTLTISGLQPEDFATYYCQYNVSPRTFGGQTKVEIK 129  
  
RESULT 4
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RESULT 3  
Q6GMX8 HUMAN  
ID Q6GMX8_HUMAN PRELIMINARY; PRT; 236 AA.  
AC Q6GMX8;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE IGKC protein.  
GN Name=IGKC;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
Batterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RG NIH MGC Project;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073764; AAH73764.1; -, mRNA.  
DR SMR; Q6GMX8; 24-235.  
DR Ensembl; ENSG00000163245; Homo sapiens.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; IG_MHC.  
DR InterPro; IPR003596; IG_v.  
DR Pfam; PF07654; C1-set; 1.  
DR SMART; SM00409; IG1; 1.  
DR SMART; SM00406; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG_LIKE; 2.  
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.  
SQ SEQUENCE 236 AA; 25707 MW; 4FCBE14B6559EFC9 CRC64;  
  
Query Match 88.7%; Score 494; DB 2; Length 236;  
Best Local Similarity 89.7%; Pred. No. 5.2e-41;  
Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;  
  
Qy 1 DIQWTSPPSSLSASVGRVTTTCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60  
Db 23 DIQWTSPPSSLSASVGRVTTTCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 82  
  
Qy 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNVSPRTFGGQTKVEIK 107  
Db 83 RFGSGSGTDFTLTISGLQPEDFATYYCQYNVSPRTFGGQTKVEIK 129  
  
RESULT 4
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Q502W4 HUMAN
ID Q502W4 HUMAN PRELIMINARY; PRT; 236 AA.
AC Q502W4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Glandular pool- thyroid;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skeletal Muscle;
RA Strausberg R.;
RL EMBL; BC005332; AAH05332.1; -; mRNA.
DR HSRF; P01834; IHEZ.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;

Query Match 88.3%; Score 492; DB 2; Length 236;
Best Local Similarity 89.7%; Pred. No. 8.2e-41;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQGISRWLANVYQOKPEKAPKSLIYAASSLSQGVPS 60
DB 23 DIQMTQSPSSLSASVGDRTVITTCRASQGISRWLANVYQOKPEKAPKSLIYAASSLSQGVPS 82

QY 61 RFSGSGSGTDFLTISGLQPEDFATYCYQYNSYPRTFGQGTKEIK 107
DB 83 RFSGSGSGTDFLTISGLQPEDFATYCYQYNSYPRTFGQGTKEIK 129

RESULT 6
KVII_HUMAN
ID KVII_HUMAN STANDARD; PRT; 117 AA.
AC P01601;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
```



```
DR SMR; P01599; 1-107.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 34
FT REGION 35 49
FT REGION 50 56
FT REGION 57 88
FT REGION 89 97
FT REGION 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11814 MW; CIAD3CB0F600FF73 CRC64;

Query Match 85.5%; Score 476; DB 1; Length 108;
Best Local Similarity 86.9%; Pred. No. 1.3e-39;
Matches 93; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQQTSPSSLSASVGDRTVITCRASQGISRWLAWYQKPKAPKSLIYAASSLSQSGVPS 60
Db 1 DIQQTSPSSLSASVGDRTVITCRASQGISRWLAWYQKPKAPKSLIYAASSLSQSGVPS 60

Qy 61 RFSGSGGTDTLTISGLQPEDFATYCCQYNSYPRTFGQGTKEIK 107
Db 61 RFSGSGGTDTLTISGLQPEDFATYCCQYNSYPRTFGQGTKEIK 107

RESULT 9
KV1V HUMAN STANDARD; PRT; 108 AA.
ID KV1V HUMAN
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE "Ig kappa chain V-I region BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240; DOI=10.1016/0161-5890(86)90173-2;
RA Dwalet F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AU) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
CC
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CC removed.
CC
CC PIR; A01878; K1HUBN.
DR HSSP; P80362; 1WTL.
DR SMR; P04430; 1-108.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Amyloid; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 34
FT REGION 35 49
FT REGION 50 56
FT REGION 57 88
FT REGION 89 97
FT REGION 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11814 MW; CIAD3CB0F600FF73 CRC64;

Query Match 85.5%; Score 476; DB 1; Length 108;
Best Local Similarity 86.9%; Pred. No. 1.3e-39;
Matches 93; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQQTSPSSLSASVGDRTVITCRASQGISRWLAWYQKPKAPKSLIYAASSLSQSGVPS 60
Db 1 DIQQTSPSSLSASVGDRTVITCRASQGISRWLAWYQKPKAPKSLIYAASSLSQSGVPS 60

Qy 61 RFSGSGGTDTLTISGLQPEDFATYCCQYNSYPRTFGQGTKEIK 107
Db 61 RFSGSGGTDTLTISGLQPEDFATYCCQYNSYPRTFGQGTKEIK 107

RESULT 9
KV1V HUMAN STANDARD; PRT; 108 AA.
ID KV1V HUMAN
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE "Ig kappa chain V-I region BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240; DOI=10.1016/0161-5890(86)90173-2;
RA Dwalet F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AU) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
CC
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; A01878; K1HUBN.
DR HSSP; P80362; 1WTL.
DR SMR; P04430; 1-108.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Amyloid; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 34
FT REGION 35 49
FT REGION 50 56
FT REGION 57 88
FT REGION 89 97
FT REGION 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11814 MW; CIAD3CB0F600FF73 CRC64;

Query Match 85.1%; Score 474; DB 2; Length 240;
Best Local Similarity 84.1%; Pred. No. 5.2e-39;
Matches 90; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQQTSPSSLSASVGDRTVITCRASQGISRWLAWYQKPKAPKSLIYAASSLSQSGVPS 60
Db 133 DIQQTSPSSLSASVGDRTVITCRASQGISRWLAWYQKPKAPKSLIYAASSLSQSGVPS 192

Qy 61 RFSGSGGTDTLTISGLQPEDFATYCCQYNSYPRTFGQGTKEIK 107
Db 193 RFSGSGGTDTLTISGLQPEDFATYCCQYNSYPRTFGQGTKEIK 239

RESULT 11
Q6GMW1 HUMAN PRELIMINARY; PRT; 236 AA.
ID Q6GMW1
AC Q6GMW1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
```

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FT REGION 24 34
FT REGION 35 49
FT REGION 50 56
FT REGION 57 88
FT REGION 89 97
FT REGION 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3PD944FE96FD37 CRC64;

Query Match 85.1%; Score 474; DB 1; Length 108;
Best Local Similarity 84.1%; Pred. No. 2.1e-39;
Matches 90; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQQTSPSSLSASVGDRTVITCRASQGISRWLAWYQKPKAPKSLIYAASSLSQSGVPS 60
Db 1 DIQQTSPSSLSASVGDRTVITCRASQGISRWLAWYQKPKAPKSLIYAASSLSQSGVPS 60

Qy 61 RFSGSGGTDTLTISGLQPEDFATYCCQYNSYPRTFGQGTKEIK 107
Db 61 RFSGSGGTDTLTISGLQPEDFATYCCQYNSYPRTFGQGTKEIK 107

RESULT 10
Q65ZC9 HUMAN PRELIMINARY; PRT; 240 AA.
ID Q65ZC9
AC Q65ZC9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=Clq/7;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13056; CAA73499.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG LIKE; 2.
FT NON_TER 1 240
FT NON_TER 240 240
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;

Query Match 85.1%; Score 474; DB 2; Length 240;
Best Local Similarity 84.1%; Pred. No. 5.2e-39;
Matches 90; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQQTSPSSLSASVGDRTVITCRASQGISRWLAWYQKPKAPKSLIYAASSLSQSGVPS 60
Db 133 DIQQTSPSSLSASVGDRTVITCRASQGISRWLAWYQKPKAPKSLIYAASSLSQSGVPS 192

Qy 61 RFSGSGGTDTLTISGLQPEDFATYCCQYNSYPRTFGQGTKEIK 107
Db 193 RFSGSGGTDTLTISGLQPEDFATYCCQYNSYPRTFGQGTKEIK 239

RESULT 11
Q6GMW1 HUMAN PRELIMINARY; PRT; 236 AA.
ID Q6GMW1
AC Q6GMW1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
```

05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

IGKC protein.
Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Spleen;
RX MDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Atschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.

RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073791; AAH73791.1; -, mRNA.
DR SMR; Q6GMW1; 24-236.
DR Ensembl; ENSG00000163245; Homo sapiens.

DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25751 MW; 5BFE6A087AFAC437 CRC64;

Query Match 84.78; Score 472; DB 2; Length 236;
Best Local Similarity 89.68; Pred. No. 8.1e-39; Indels 0; Gaps 0;
Matches 95; Conservative 1; Mismatches 10;

QY 2 IQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPSR 61
DB 24 IQMTQSPSSLSASVGDRTVITCRASQGISNDLGMWYQOKPEKAPKSLIYAASSLSQGVPSR 83

QY 62 FSGSGSGTDTLTITISGLQPEDPATYCCQYNSYPRTFGGQTKVEIK 107
DB 84 FSGSGSGTDTLTITISGLQPEDPATYCCQYNSYPRTFGGQTKVEIK 129

RESULT 12
Q6PIH7 HUMAN
ID Q6PIH7 HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6PIH7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
IGKC protein.
Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Lung;
RX MDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Atschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.

RC TISSUE=Lung;
RG NIH MGC Project;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034141; AAH34141.1; -, mRNA.
DR HSP; P01607; IAR2.
DR SMR; Q6PIH7; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.

DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;

Query Match 84.68; Score 471; DB 2; Length 236;
Best Local Similarity 86.98; Pred. No. 1e-38; Indels 0; Gaps 0;
Matches 93; Conservative 4; Mismatches 10;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
DB 23 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 82

QY 61 RFGSGSGTDTLTITISGLQPEDPATYCCQYNSYPRTFGGQTKVEIK 107
DB 83 RFGSGSGTDTLTITISGLQPEDPATYCCQYNSYPRTFGGQTKVEIK 129

RESULT 13
KVIF HUMAN
ID KVIF HUMAN STANDARD; PRT; 108 AA.
AC P01598;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN (1)
RP PROTEIN SEQUENCE.
RX MEDLINE=71064023; PubMed=5489770;
RA Gottleb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT acid sequence of the light chain."
RL Biochemistry 9:3155-3161(1970).
RN (2)
RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds."
RL Biochemistry 9:3188-3196(1970).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein.
CC -----
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CC -----
DR PIR; A90562; KIHUEU.
DR HSSP; P01607; 1BWV.
DR SMR; P01598; 1-107.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; Ig_v.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 34 Complementarity-determining-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Framework-3.
FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 107 Framework-4.
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;
Query Match 84.0%; Score 468; DB 1; Length 108;
Best Local Similarity 83.2%; Pred. No. 8.4e-39;
Matches 89; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRLWYQQKPEKAPKSLIYAASSLSQGVPS 60
DB 1 DIQMTQSPSTLSASVGDRTVITCRASQGISRLWYQQKPEKAPKSLIYAASSLSQGVPS 60
QY 61 RFGSGSGTDFLTISGLQPEDFATYYCQYNSYPRTEGQTKVEIK 107
DB 61 RFGSGSGTDFLTISGLQPEDFATYYCQYNSYPRTEGQTKVEIK 107
RESULT 14
KVIL_HUMAN
ID KVIL_HUMAN STANDARD; PRT; 108 AA.
AC P01604;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region Kue.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN (1)
RP PROTEIN SEQUENCE.
RX MEDLINE=79237924; PubMed=112021;
RA Eulitz M., Kley H.-P., Zeitler H.-J.;
RT "The primary structure of the Bence-Jones protein Kue. The amino acid
RT sequence of the variable part of a human L-chain of the kappa-type.";
RL Hoppe-Seyler's Z. Physiol. Chem. 360:725-734(1979).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC removed.
CC -----
DR PIR; A01870; KIHUKU.
DR HSSP; P01607; 1BWV.
DR SMR; P01604; 1-108.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IG_v.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 34 Complementarity-determining-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Framework-3.
FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 107 Framework-4.
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 12127 MW; 906679A5D9084E98 CRC64;
Query Match 83.8%; Score 467; DB 1; Length 108;
Best Local Similarity 81.3%; Pred. No. 1.1e-38;
Matches 87; Conservative 11; Mismatches 9; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRLWYQQKPEKAPKSLIYAASSLSQGVPS 60
DB 1 DIQMTQSPSTQPSVGDRTVITCRASQGISRLWYQQKPEKAPKSLIYAASSLSQGVPS 60
QY 61 RFGSGSGTDFLTISGLQPEDFATYYCQYNSYPRTEGQTKVEIK 107
DB 61 RFGSGSGTDFLTISGLQPEDFATYYCQYNSYPRTEGQTKVEIK 107
RESULT 15
KVIR_HUMAN
ID KVIR_HUMAN STANDARD; PRT; 108 AA.
AC P01610;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN (1)

RP PROTEIN SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
RT (protein WEA) with antibody activity against 3,4-pyruvylated galactose
RT in Klebsiella polysaccharides K30 and K33.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -1- MISCELLANEOUS: This chain was obtained from a monoclonal antibody
CC against 3,4-pyruvylated galactose and isolated from a patient with
CC Waldenström's macroglobulinemia.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A01876; KIHUME.
DR HSP; P80362; 1WTL.
DR SMR; P01610; 1-108.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Monoclonal antibody.
FT REGION 1 23 Framework-1.
FT REGION 24 34 Complementarity-determining-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Framework-3.
FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

Query Match 83.5%; Score 465; DB 1; Length 108;
Best Local Similarity 84.1%; Pred. No. 1.7e-38;
Matches 90; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDVRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 1 DIQWTQSPSSLSASVGDVRVTITCRASQGISRWLAWYQOKPEKAPKSLIYGATSLQGVPS 60

Qy 61 RFGSGSGTDTLTITISGLQPEDFATYICQYNVYPTFGQTKVEIK 107
Db 61 RFGSGSGTDTLTITISGLQPEDFATYICQYNVYPTFGQTKVEIK 107

Search completed: December 3, 2005, 14:32:20
Job time : 189.669 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 14:10:00 ; Search time 182.992 Seconds
(without alignments)
256.916 Million cell updates/sec

Title: US-10-769-144-8

Perfect score: 557

Sequence: 1 DIQWTQSPSSLSASVGRVT.....CQQNSYPTFTGQTKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 4393781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: geneseqp1980s.*
- 2: geneseqp1990s.*
- 3: geneseqp2000s.*
- 4: geneseqp2001s.*
- 5: geneseqp2002s.*
- 6: geneseqp2003as.*
- 7: geneseqp2003bs.*
- 8: geneseqp2004s.*
- 9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	557	100.0	107	5	AAM48004 Human mon
2	557	100.0	107	8	ADR46825 Human ant
3	557	100.0	233	8	ADR46823 Human ant
4	557	100.0	411	8	ADR46829 Human pbl
5	538	96.6	107	4	AAB67511 Light cha
6	538	96.6	107	9	ADY70214 Human mon
7	538	96.6	108	7	ADY11407 18B2 anti
8	538	96.6	214	7	ADY11431 18B2 anti
9	537	96.4	107	9	ADY26773 Anti-NGF
10	535	96.1	107	4	AAB72880 Human ant
11	535	96.1	107	8	ADO36490 Human ant
12	535	96.1	107	8	ADO36502 Human ant
13	535	96.1	107	8	ADO36494 Human ant
14	535	96.1	234	9	AEB48576 Human kap
15	535	96.1	236	9	ADW86270 Anti-huma
16	535	96.1	239	9	AEB48570 Human kap
17	535	96.1	290	9	AEB48564 Human kap
18	532	95.3	107	9	ADY70210 Human mon
19	531	95.3	107	8	ADT88867 Human IGF
20	531	95.3	107	8	ADT88874 Human IGF
21	531	95.3	107	9	AEB01063 Human IGF
22	530	95.2	107	4	AAB72882 Human ant
23	530	95.2	107	4	AAB82890 Anti-huma
24	530	95.2	107	9	ADW07059 Anti-Psaa

25	529	95.0	107	8	ADT88865	Adt88865 Human IGF
26	529	95.0	107	8	ADT88863	Adt88863 Human IGF
27	529	95.0	108	5	AAU76522	Aau76522 Anti-Inte
28	524	94.1	108	7	ADF11399	Adf11399 2E11 anti
29	524	94.1	214	7	ADF11423	Adf11423 2E11 anti
30	523	93.9	224	4	AAB75040	Aab75040 TRO005 Hu
31	521	93.5	128	7	ABU64274	Abu64274 Human C40
32	519	93.2	107	6	AAB38063	Aab38063 Human 5F1
33	518	93.0	224	4	AAB75044	Aab75044 TRO005 Hu
34	508	91.2	107	8	ADP22406	Adp22406 Human ant
35	508	91.2	129	7	ADZ57711	Adz57711 Germline
36	506	90.8	107	7	ADK18619	Adk18619 Anti-huma
37	506	90.8	107	7	ADK18794	Adk18794 Anti-huma
38	506	90.8	107	8	ADL25454	Adl25454 Human mAb
39	506	90.8	124	3	RAY56723	Ray56723 Amino aci
40	505	90.7	127	6	AAE37206	Aae37206 Human AB-
41	505	90.7	127	9	AEA16227	Aea16227 Anti-huma
42	504	90.5	107	8	ADP22216	Adp22216 Human ant
43	502	90.1	108	9	AEA41087	Aea41087 Germline
44	502	90.1	127	6	AAE37204	Aae37204 Human AB-
45	502	90.1	127	9	AEA16223	Aea16223 Anti-huma

ALIGNMENTS

RESULT 1
AAM48004
ID AAM48004 standard; protein, 107 AA.
XX
AC AAM48004;
XX
DT 08-MAR-2002 (first entry)
XX
DE Human monoclonal antibody B11 variable light chain protein.
XX
KW Human; monoclonal antibody; B11; antigen binding portion; dendritic cell;
KW mannose receptor; growth; cytolysis; pathogen; virus; bacterium;
KW autoimmune disease; inflammatory disorder; rheumatoid arthritis;
KW multiple sclerosis; diabetes mellitus; immunomodulatory;
KW antiinflammatory; antirheumatic; antiarthritic; neuroprotective;
KW antidiabetic; antianemic; endocrine; dermatological; antithyroid;
KW uropathic; ophthalmological; muscular.
XX
OS Homo sapiens.
XX
PN WO200185798-A2.
XX
PD 15-NOV-2001.
XX
PF 08-MAY-2001; 2001WO-US015114.
XX
PR 08-MAY-2000; 2000US-0203126P.
PR 07-SEP-2000; 2000US-0230739P.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Deo YM, Keler T;
XX
DR WPI; 2002-089788/12.
XX
DR N-PSDB; ABA06023.
XX
PT New human monoclonal antibodies specific for dendritic cells, useful for
PT inhibiting growth or inducing cytolysis of a dendritic cell and treating
PT or preventing a dendritic cell mediated disease, e.g., autoimmune
XX
PS Example 2; Fig 13; 95pp; English.
XX
CC The invention relates to human monoclonal antibodies or their antigen
CC binding portions that specifically bind to dendritic cells and has one or
CC more of the following characteristics: (a) a binding affinity constant to
CC a dendritic cell of at least about 10 to the power 7 M-1; (b) the ability

CC to opsonise a dendritic cell; (c) the ability to internalise after
 CC binding to dendritic cells; or (d) the ability to activate dendritic
 CC cells. The isolated human monoclonal antibody or its antigen binding
 CC portion may also have any of the following characteristics: (a) mediates
 CC cytolysis of dendritic cells in the presence of human effector cells; or
 CC (b) inhibits growth of dendritic cells. The antibodies or its antigen
 CC binding portion, binds to and blocks the human mannose receptor on
 CC dendritic cells. The antibodies have immunomodulatory, antiinflammatory,
 CC antirheumatic, antarthritic, neuroprotective, antidiabetic, antianemic,
 CC endocrine, dermatological, antithyroid, uropathic, ophthalmological and
 CC muscular activity. The antibodies or their antigen-binding fragments are
 CC useful for inhibiting growth of a dendritic cell, inducing cytolysis of a
 CC dendritic cell, treating or preventing a dendritic cell mediated disease,
 CC detecting the presence of a dendritic cell, targeting an antigen to a
 CC dendritic cell and preventing binding of a pathogen (a virus or a
 CC bacterium) to human mannose receptor on dendritic cells. In particular,
 CC the antibodies may be used to treat, autoimmune disease, graft versus
 CC host disease, immune system or inflammatory disorders (e.g. rheumatoid
 CC arthritis), multiple sclerosis, diabetes mellitus, myasthenia gravis,
 CC pernicious anaemia, Addison's disease, lupus erythematosus, Reiter's
 CC syndrome and Graves disease. The present sequence is that of the human
 CC monoclonal antibody B11 variable light chain, useful to the invention
 XX
 SQ Sequence 107 AA;

Query Match 100.0%; Score 557; DB 5; Length 107;
 Best Local Similarity 100.0%; Pred. No. 5e-36;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQWTQSPSSLSASVGRVITTCRASQGISRWLAWYQKPKAPKSLIYAASSLSQGVPS 60
 Db 1 DIQWTQSPSSLSASVGRVITTCRASQGISRWLAWYQKPKAPKSLIYAASSLSQGVPS 60
 Qy 61 RFGSGSGTDFTLTISGLQPEDFATYCCQYNSYPRTFGGTKVIEK 107
 Db 61 RFGSGSGTDFTLTISGLQPEDFATYCCQYNSYPRTFGGTKVIEK 107

RESULT 2
 ADR46825
 ID ADR46825 standard; protein; 107 AA.

AC ADR46825;
 DT 18-NOV-2004 (first entry)
 XX Human antibody B11 light chain variable region protein SEQ ID NO:8.
 XX molecular conjugate; monoclonal antibody; human antigen presenting cell;
 XX antigen presenting cell; APC; human; beta human chorionic gonadotropin;
 XX betahCG; beta chorionic gonadotropin; antibody;
 XX T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
 XX immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
 XX CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
 XX melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
 XX antibody B11; light chain variable region.
 XX Homo sapiens.
 XX WO2004074432-A2.
 XX
 XX 02-SEP-2004.
 XX 30-JAN-2004; 2004WO-US002725.
 XX
 XX 31-JAN-2003; 2003US-0443979P.
 XX (MEDA-) MEDAREX INC.

XX Keler T, Endres M, He L, Ramakrishna V;
 XX WPI; 2004-635555/61.
 XX N-PSDB; ADR46824.

XX New molecular conjugate having a monoclonal antibody that binds to human
 PT APCs linked to a beta human chorionic gonadotropin, useful for inducing a
 PT cytotoxic T cell response in cancers and infectious diseases.
 XX
 PS Claim 11; SEQ ID NO 8; 82pp; English.

XX The present invention describes a molecular conjugate comprising a
 CC monoclonal antibody that binds to human antigen presenting cells (APCs)
 CC linked to beta human chorionic gonadotropin (betahCG), where the antibody
 CC comprises a heavy and/or light chain variable region derived from a human
 CC VH5-51 or VK-L15 germ-line sequence with the 98 or 95 amino acid sequences
 CC of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
 CC described: (1) a molecular conjugate comprising a human antibody heavy
 CC chain and a human antibody light chain, where either or both chains are
 CC linked to betahCG; (2) a molecular conjugate comprising a human single
 CC chain antibody that binds to human APCs linked to betahCG, where the
 CC conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
 CC (ADR46829); (3) a composition comprising any of the molecular conjugates
 CC as described above, and a carrier, optionally in combination with an
 CC adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
 CC against betahCG, comprising contacting any of the molecular conjugates
 CC described above with APCs such that the antigen is processed and
 CC presented to T cells in a manner which induces or enhances a T cell-
 CC mediated response against the antigen; (5) immunising a subject
 CC comprising administering any of the molecular conjugates described above,
 CC optionally in combination with an adjuvant, a cytokine which stimulates
 CC proliferation of dendritic cells and/or an immunostimulatory agent; and
 CC (6) inducing or enhancing a cytotoxic T cell response against an antigen,
 CC comprising forming a conjugate of the antigen and a monoclonal antibody
 CC which binds to APCs, and contacting the conjugate either in vivo or ex
 CC vivo with APCs such that the antigen is internalised, processed and
 CC presented to T cells in a manner which induces or enhances a cytotoxic T
 CC cell response against the antigen. The molecular conjugate has
 CC cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
 CC virucide and antimalarial activities, and can be used as a CD8 agonist,
 CC and in vaccines. The methods and compositions of the present invention
 CC are useful for inducing a cytotoxic T cell response, and in particular
 CC for treating autoimmune disorders, cancers and infectious diseases by
 CC eliciting a potent antigen-specific cytotoxic T lymphocyte response,
 CC including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
 CC herpes. The present sequence represents a human antibody B11 light chain
 CC variable region, which is used in the exemplification of the present
 CC invention.

XX Sequence 107 AA;

Query Match 100.0%; Score 557; DB 8; Length 107;
 Best Local Similarity 100.0%; Pred. No. 5e-36;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQWTQSPSSLSASVGRVITTCRASQGISRWLAWYQKPKAPKSLIYAASSLSQGVPS 60
 Db 1 DIQWTQSPSSLSASVGRVITTCRASQGISRWLAWYQKPKAPKSLIYAASSLSQGVPS 60
 Qy 61 RFGSGSGTDFTLTISGLQPEDFATYCCQYNSYPRTFGGTKVIEK 107
 Db 61 RFGSGSGTDFTLTISGLQPEDFATYCCQYNSYPRTFGGTKVIEK 107

RESULT 3
 ADR46823
 ID ADR46823 standard; protein; 233 AA.

XX ADR46823;
 XX
 XX 18-NOV-2004 (first entry)
 DT Human antibody B11 light chain variable region protein SEQ ID NO:6.
 XX molecular conjugate; monoclonal antibody; human antigen presenting cell;
 DE antigen presenting cell; APC; human; beta human chorionic gonadotropin;
 XX betahCG; beta chorionic gonadotropin; antibody;

T cell-mediated immune response; immunisation; cytostatic; antimicrobial; immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial; CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease; melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes; antibody B11; light chain variable region.

Homo sapiens.

WO2004074432-A2.

02-SEP-2004.

30-JAN-2004; 2004WO-US002725.

31-JAN-2003; 2003US-0443979P.

(MEDA-) MEDAREX INC.

Keler T, Endres M, He L, Ramakrishna V;

WPI; 2004-635555/61.

N-PSDB; ADR46822.

New molecular conjugate having a monoclonal antibody that binds to human APCs linked to a beta human chorionic gonadotropin, useful for inducing a cytotoxic T cell response in cancers and infectious diseases.

Claim 14; SEQ ID NO 6; 82pp; English.

The present invention describes a molecular conjugate comprising a monoclonal antibody that binds to human antigen presenting cells (APCs) linked to beta human chorionic gonadotropin (betahCG), where the antibody comprises a heavy and/or light chain variable region derived from a human VH5-51 or Vk-L15 germline sequence with the 98 or 95 amino acid sequences of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also described: (1) a molecular conjugate comprising a human antibody heavy chain and a human antibody light chain, where either or both chains are linked to betahCG; (2) a molecular conjugate comprising a human single chain antibody that binds to human APCs linked to betahCG, where the conjugate comprises the 411 amino acid sequence of SEQ ID NO:12 (ADR46829); (3) a composition comprising any of the molecular conjugates as described above, and a carrier, optionally in combination with an adjuvant; (4) inducing or enhancing a T cell-mediated immune response, against betahCG, comprising contacting any of the molecular conjugates described above with APCs such that the antigen is processed and presented to T cells in a manner which induces or enhances a T cell-mediated response against the antigen; (5) immunising a subject comprising administering any of the molecular conjugates described above, optionally in combination with an adjuvant, a cytokine which stimulates proliferation of dendritic cells and/or an immunostimulatory agent; and (6) inducing or enhancing a cytotoxic T cell response against an antigen, comprising forming a conjugate of the antigen and a monoclonal antibody which binds to APCs, and contacting the conjugate either in vivo or ex vivo with APCs such that the antigen is internalised, processed and presented to T cells in a manner which induces or enhances a cytotoxic T cell response against the antigen. The molecular conjugate has cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic, virucide and antimalarial activities, and can be used as a CD8 agonist, and in vaccines. The methods and compositions of the present invention are useful for inducing a cytotoxic T cell response, and in particular for treating autoimmune disorders, cancers and infectious diseases by eliciting a potent antigen-specific cytotoxic T lymphocyte response, including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and herpes. The present sequence represents a human antibody B11 light chain variable region, which is used in the exemplification of the present invention.

Sequence 233 AA;

Query Match 100.0%; Score 557; DB 8; Length 233;
 Best Local Similarity 100.0%; Pred. No. 1e-35;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVSGDRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60
 Db 20 DIQMTQSPSSLSASVSGDRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 79
 Qy 61 RFGSGSGTPTLTISGLQPEDFATYYCQQVNSYPRTFGGQTKVEIK 107
 Db 80 RFGSGSGTPTLTISGLQPEDFATYYCQQVNSYPRTFGGQTKVEIK 126

RESULT 4

ADR46829

ID ADR46829 standard; protein; 411 AA.

XX

AC ADR46829;

XX

DT 18-NOV-2004 (first entry)

XX

DE Human pB11-betahCG molecular conjugate protein SEQ ID NO:12.

XX

KW molecular conjugate; monoclonal antibody; human antigen presenting cell;
 KW antigen presenting cell; APC; human; beta human chorionic gonadotropin;
 KW betahCG; beta chorionic gonadotropin; antibody;
 KW T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
 KW immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
 KW CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
 KW melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
 KW antibody B11; pB11-betahCG molecular conjugate; fusion protein.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO2004074432-A2.

XX

PD 02-SEP-2004.

XX

PF 30-JAN-2004; 2004WO-US002725.

XX

PR 31-JAN-2003; 2003US-0443979P.

XX

PA (MEDA-) MEDAREX INC.

XX

PI Keler T, Endres M, He L, Ramakrishna V;

XX

DR WPI; 2004-635555/61.

XX

DR N-PSDB; ADR46828.

XX

PT New molecular conjugate having a monoclonal antibody that binds to human APCs linked to a beta human chorionic gonadotropin, useful for inducing a cytotoxic T cell response in cancers and infectious diseases.

XX

PS Claim 16; SEQ ID NO 12; 82pp; English.

XX

CC The present invention describes a molecular conjugate comprising a monoclonal antibody that binds to human antigen presenting cells (APCs) linked to beta human chorionic gonadotropin (betahCG), where the antibody comprises a heavy and/or light chain variable region derived from a human VH5-51 or Vk-L15 germline sequence with the 98 or 95 amino acid sequences of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also described: (1) a molecular conjugate comprising a human antibody heavy chain and a human antibody light chain, where either or both chains are linked to betahCG; (2) a molecular conjugate comprising a human single chain antibody that binds to human APCs linked to betahCG, where the conjugate comprises the 411 amino acid sequence of SEQ ID NO:12 (ADR46829); (3) a composition comprising any of the molecular conjugates as described above, and a carrier, optionally in combination with an adjuvant; (4) inducing or enhancing a T cell-mediated immune response, against betahCG, comprising contacting any of the molecular conjugates described above with APCs such that the antigen is processed and presented to T cells in a manner which induces or enhances a T cell-mediated response against the antigen; (5) immunising a subject comprising administering any of the molecular conjugates described above, optionally in combination with an adjuvant, a cytokine which stimulates proliferation of dendritic cells and/or an immunostimulatory agent; and (6) inducing or enhancing a cytotoxic T cell response against an antigen, comprising forming a conjugate of the antigen and a monoclonal antibody which binds to APCs, and contacting the conjugate either in vivo or ex vivo with APCs such that the antigen is internalised, processed and presented to T cells in a manner which induces or enhances a cytotoxic T cell response against the antigen. The molecular conjugate has cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic, virucide and antimalarial activities, and can be used as a CD8 agonist, and in vaccines. The methods and compositions of the present invention are useful for inducing a cytotoxic T cell response, and in particular for treating autoimmune disorders, cancers and infectious diseases by eliciting a potent antigen-specific cytotoxic T lymphocyte response, including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and herpes. The present sequence represents a human antibody B11 light chain variable region, which is used in the exemplification of the present invention.

(6) inducing or enhancing a cytotoxic T cell response against an antigen, comprising forming a conjugate of the antigen and a monoclonal antibody which binds to APCs, and contacting the conjugate either in vivo or ex vivo with APCs such that the antigen is internalised, processed and presented to T cells in a manner which induces or enhances a cytotoxic T cell response against the antigen. The molecular conjugate has cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic, virucide and antimalarial activities, and can be used as a CD8 agonist, are useful for inducing a cytotoxic T cell response, and in particular for treating autoimmune disorders, cancers and infectious diseases by eliciting a potent antigen-specific cytotoxic T lymphocyte response. including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and herpes. The present sequence represents a human p11-betaHCG molecular conjugate, which is used in the exemplification of the present invention.

SQ Sequence 411 AA;

Query Match 100.0%; Score 557; DB 8; Length 411;
 Best Local Similarity 100.0%; Pred. No. 1.8e-35;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 79

Qy 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYPTFGQGTKEIK 107

Db 80 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYPTFGQGTKEIK 126

RESULT 5

AAB67511

ID AAB67511 standard; peptide; 107 AA.

AC AAB67511;

DT 29-MAY-2001 (first entry)

DE Light chain variable region of anti-CTLA-4 antibody 1E2.

KW Complementarity determining region; CDR; immune response; antibody;
 KW cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
 KW autoimmune disease; infectious disease; inflammation; allergy;
 KW rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
 KW multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
 KW transplant rejection; graft versus host disease.

OS Homo sapiens.

PH Key Location/Qualifiers

FT Region 24..34

FT /note= "CDR1"

FT Region 50..66

FT /note= "CDR2"

FT Region 89..97

FT /note= "CDR3"

XX WO200114424-A2.

XX 01-MAR-2001.

XX 24-AUG-2000; 2000WO-US023356.

XX 24-AUG-1999; 99US-0150452P.

XX (MEDA-) MEDAREX INC.

XX Korman AJ, Halk EL, Lonberg N;

XX WPI; 2001-202933/20.

XX Novel human sequence antibody that binds to human cytotoxic T lymphocyte

PT associated antigen-4, useful for inducing, augmenting or prolonging
 PT immune response to antigen or for suppressing immune response in patient.
 XX Claim 27; Fig 7; 127pp; English.

XX The present sequence represents the light chain variable region of human
 CC antibody 1E2. This antibody specifically binds to human cytotoxic T
 CC lymphocyte associated antigen-4 (CTLA-4). Such antibodies are used in
 CC methods for inducing, augmenting or prolonging an immune response to an
 CC antigen in a patient, where the antibodies block binding of human CTLA-4
 CC to human B7 ligands. The antibodies are also useful for treating
 CC autoimmune disease in a subject caused or exacerbated by increased
 CC activity of T cells and for treating prostate cancer, melanoma or
 CC epithelial cancer. A polyvalent or polyclonal antibody preparation
 CC comprising two antibodies of the invention are useful for suppressing a
 CC immune response in a patient. They are used for treating cancer,
 CC infectious diseases and promoting beneficial autoimmune reactions. The
 CC treatment of diseases with inflammatory or allergic components. The
 CC polyvalent or polyclonal preparations are useful for treating autoimmune
 CC diseases such as rheumatoid arthritis, myasthenia gravis and lupus
 CC erythematosus, multiple sclerosis, insulin-dependent diabetes mellitus,
 CC transplant rejection, and inflammation, graft versus host disease
 XX Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34;
 Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60
 Db 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYPTFGQGTKEIK 107

Db 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYPTFGQGTKEIK 107

RESULT 6

ADY70214

ID ADY70214 standard; protein; 107 AA.

XX AC ADY70214;

DT 02-JUN-2005 (first entry)

XX Human monoclonal antibody 5D5 VK region.

XX vaccine; antibacterial; monoclonal antibody; protective antigen;
 KW lethal factor; toxin; anthrax infection; screening; detection; 5D5;
 KW light chain variable region.

OS Homo sapiens.

XX Synthetic.

PH Key Location/Qualifiers

FT Region 24..34

FT /label= CDR1

FT /note= "complementarity determining region"

FT Region 50..56

FT /label= CDR2

FT /note= "complementarity determining region"

FT Region 89..97

FT /label= CDR3

FT /note= "complementarity determining region"

XX WO2005023177-A2.

XX 17-MAR-2005.

XX 21-MAY-2004; 2004WO-US016213.

XX 21-MAY-2003; 2003US-0472636P.

PR 16-OCT-2003; 2003US-0512336P.
XX (MEDA-) MEDAREX INC.
XX Keler T, Blanset D, Vitale LA, Lowy I, Srinivasan M;
XX WPI; 2005-214725/22.
DR N-PSDB; ADY70213.
XX
XX New human monoclonal antibody that binds to Bacillus anthracis protective
PT antigen and neutralizes a Bacillus anthracis toxin, useful in preparing a
PT composition for treating or preventing anthrax infection.
XX
XX Claim 10; SEQ ID NO 18; 119pp; English.
XX
XX This invention describes a novel human monoclonal antibody which binds to
CC Bacillus anthracis protective antigen with an affinity of at least 10⁻⁷ M
CC -1 and neutralizes a Bacillus anthracis lethal factor toxin at an ED-50
CC of 5 microg/ml or less in a toxin neutralization assay. The invention
CC also describes: 1) an expression vector; 2) a transfectoma comprising the
CC expression vector; 3) a transgenic non-human animal that expresses the
CC human monoclonal antibody and that has a genome comprising a human heavy
CC chain transgene or transchromosome and a human light chain transgene or
CC transchromosome; 4) an immunoconjugate comprising the human monoclonal
CC antibody, linked to a therapeutic agent chosen from a cytotoxin or
CC radioisotope; 5) a pharmaceutical composition comprising the
CC immunoconjugate or human monoclonal antibody and a carrier or an
CC additional therapeutic agent, comprising a protective antigen vaccine or
CC a second antibody against anthrax bacteria, spores, lethal factor or
CC edema factor, Fab, F(ab')₂, Fv or single chain Fv fragment of the second
CC antibody; 6) a hybridoma that produces a detectable amount of the human
CC monoclonal antibody; 7) a method of producing the human monoclonal
CC antibody; 8) a method of inhibiting a physiological activity of Bacillus
CC anthracis protective antigen in a cell susceptible to anthrax infection;
CC 9) a method of neutralizing a Bacillus anthracis toxin in a cell
CC susceptible to anthrax infection comprising immunizing the transgenic non
CC -human animal with Bacillus anthracis protective antigen or a cell
CC expressing Bacillus anthracis protective antigen, so that antibodies are
CC produced by B cells of the animal, isolating B cells of the animal and
CC fusing the B cells with myeloma cells to form immortal hybridoma cells
CC that secrete the antibody; 10) a method of treating or preventing anthrax
CC infection in a host infected with Bacillus anthracis; 11) a method of
CC detecting the presence of Bacillus anthracis protective antigen in a
CC sample; 12) a method of treating or preventing anthrax infection in a
CC patient and 13) a method of screening for an antibody against anthrax
CC protective antigen. The human monoclonal antibody comprises human IgG1 or
CC IgG3 heavy chain variable region and a human kappa light chain variable
CC and their conservative sequence modifications. The human monoclonal
CC antibody is a Fab fragment or a single chain antibody (scFv) and is
CC produced by a hybridoma, which is prepared from a B cell obtained from a
CC transgenic non-human animal having a genome comprising a human heavy
CC chain transgene or transchromosome and a human light chain transgene or
CC transchromosome fused to an immortalized cell. The heavy or light chain
CC variable region comprises FR1, FR2, FR3, CDR2, FR3, CDR3 or FR4. The
CC heavy chain variable region having FR1, FR2, FR3 or FR4 sequences are
CC derived from the human heavy chain VH3-33 or VH3-7 germline sequences.
CC The light chain variable region having FR1, FR2, FR3 or FR4 sequences are
CC derived from the human light chain L15, L18 or A27 germline sequences.
CC The ability of the antibody to neutralize the toxin requires binding to
CC Fc receptor. This sequence represents the human monoclonal antibody 5D5
CC variable region light chain comprising a L15 V-segment and a JK4 J-
XX segment.

XX Sequence 107 AA;

Query Match 96.6%; Score 538; DB 9; Length 107;
Best Local Similarity 97.2%; Pred. No. 1.5e-34;
Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60

QY 61 RFGSGSGTDTLTISGLQPEDFATYYCQYNSYPRTFGGQTKVEIK 107
DB 61 RFGSGSGTDTLTISGLQPEDFATYYCQYNSYPRTFGGQTKVEIK 107

RESULT 7

ADF11407
ID ADF11407 standard; protein; 108 AA.

XX AC ADF11407;

XX DT 12-FEB-2004 (first entry)

XX DE 18B2 anti-OPGL antibody kappa chain variable region SEQ ID NO:20.

XX KW human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;
XX KW osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;
XX KW osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.

XX OS Homo sapiens.

XX FN WO2003086289-A2.

XX XX 23-OCT-2003.

XX PF 07-APR-2003; 2003WO-US010749.

XX PR 05-APR-2002; 2002US-0370407P.

XX PA (AMGE-) AMGEN INC.

XX FI Boyle WJ, Medlock E, Sullivan JK, Elliott RL, Martin F, Huang H;

XX DR WPI; 2003-845253/78.

XX DR N-PSDB; ADF11406.

XX PT New isolated antibody that specifically binds osteoprotegerin ligand,
XX PT useful for diagnosing or treating bone disorders, such as osteoporosis,
XX PT bone loss from arthritis, Paget's disease or osteopenia.

XX PS Claim 8; SEQ ID NO 20; 156pp; English.

XX CC The present invention describes an isolated human antibody (I) that
XX CC specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a
XX CC pharmaceutical composition comprising a pharmaceutical carrier and a
XX CC therapeutic amount of (I); (2) methods of treating an osteopenic disorder
XX CC in a patient, comprising administering to a patient the pharmaceutical
XX CC composition of (I) or a pharmaceutical amount of (I); and (3) a method
XX CC for detecting OPGL in a biological sample, comprising contacting the
XX CC sample with (I) under conditions that allow for binding of the antibody
XX CC to OPGL, and measuring the level of bound antibody in the sample. (I) has
XX CC osteopathic, antiarthritic and cytostatic activities, and can be used in
XX CC gene therapy. The composition and methods are useful in diagnosing or
XX CC treating bone disorders, such as osteoporosis, bone loss from arthritis,
XX CC Paget's disease or osteopenia. The antibody (I) may also be used for
XX CC detecting OPGL in biological samples and in identifying cells or tissues
XX CC that produce the protein. The present sequence represents a sequence
XX CC which is used in the exemplification of the present invention.

XX SQ Sequence 108 AA;

Query Match 96.6%; Score 538; DB 7; Length 108;
Best Local Similarity 97.2%; Pred. No. 1.5e-34;
Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60

QY 61 RFGSGSGTDTLTISGLQPEDFATYYCQYNSYPRTFGGQTKVEIK 107
DB 61 RFGSGSGTDTLTISGLQPEDFATYYCQYNSYPRTFGGQTKVEIK 107

```
RESULT 8
ADFL1431
ID ADFL1431 standard; protein; 214 AA.
XX AC ADFL1431;
XX AC ADFL1431;
XX DE 12-FEB-2004 (first entry)
XX DT 1882 anti-OPGL antibody light chain SEQ ID NO:44.
XX KW human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;
XX KW osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;
XX KW osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.
XX OS Homo sapiens.
XX PN WO2003086289-A2.
XX PD 23-OCT-2003.
XX PF 07-APR-2003; 2003WO-US010749.
XX PR 05-APR-2002; 2002US-0370407P.
XX PA (AMGE-) AMGEN INC.
XX PI Boyle WJ, Medlock E, Sullivan JK, Elliott RL, Martin F, Huang H;
XX DR WPI; 2003-845253/78.
XX DR N-PSDB; ADFL1430.
XX PT New isolated antibody that specifically binds osteoprotegerin ligand,
XX PT useful for diagnosing or treating bone disorders, such as osteoporosis,
XX PT bone loss from arthritis, Paget's disease or osteopenia.
XX PS Claim 18; SEQ ID NO 44; 156pp; English.
XX CC The present invention describes an isolated human antibody (I) that
XX CC specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a
XX CC pharmaceutical composition comprising a pharmaceutical carrier and a
XX CC therapeutic amount of (I); (2) methods of treating an osteopenic disorder
XX CC in a patient, comprising administering to a patient the pharmaceutical
XX CC composition of (1) or a pharmaceutical amount of (I); and (3) a method
XX CC for detecting OPGL in a biological sample, comprising contacting the
XX CC sample with (I) under conditions that allow for binding of the antibody
XX CC to OPGL, and measuring the level of bound antibody in the sample. (I) has
XX CC osteopathic, antiarthritic and cytostatic activities, and can be used in
XX CC gene therapy. The composition and methods are useful in diagnosing or
XX CC treating bone disorders, such as osteoporosis, bone loss from arthritis,
XX CC Paget's disease or osteopenia. The antibody (I) may also be used for
XX CC detecting OPGL in biological samples and in identifying cells or tissues
XX CC that produce the protein. The present sequence represents a sequence
XX CC which is used in the exemplification of the present invention.
XX SQ Sequence 214 AA;
Query Match 96.6%; Score 538; DB 7; Length 214;
Best Local Similarity 97.2%; Pred. No. 2.9e-34;
Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 DIQMTQSPSSLSASVGRVITTCRASQGISRLAWYQQKPKAPKSLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVITTCRASQGISRLAWYQQKPKAPKSLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDFTLISGLQPEDFATYICQYNSVPRTFGGQTKVEIK 107
Db 61 RFGSGSGTDFTLISGLQPEDFATYICQYNSVPRTFGGQTKVEIK 107
RESULT 9
ADY26773
ID ADY26773 standard; protein; 107 AA.
XX AC ADY26773;
XX DT 19-MAY-2005 (first entry)
XX DE Anti-NGF-antibody light chain variable region SEQ ID NO 88.
XX KW analgesic; gene therapy; antibody engineering; pharmaceutical; pain;
XX KW neurological disease; NGF; nerve growth factor;
XX KW light chain variable region.
XX OS Homo sapiens.
XX PN WO2005019266-A2.
XX PD 03-MAR-2005.
XX PF 15-JUL-2004; 2004WO-US022876.
XX PR 15-JUL-2003; 2003US-0487431P.
XX PA (AMGE-) AMGEN INC.
XX PI Wild KD, Treanor JJS, Huang H, Inoue H, Zhang TJ, Martin F;
XX DR WPI; 2005-202606/21.
XX PT New human anti-nerve growth factor (NGF) neutralizing antibodies useful
XX PT for manufacturing a medicament for treating painful disorders (e.g. acute
XX PT pain) or conditions associated with increased expression or sensitivity
XX PT to NGF.
XX PS Claim 33; SEQ ID NO 88; 190pp; English.
XX CC The invention describes an isolated human antibody that interacts with or
XX CC binds specifically to human nerve growth factor (NGF) and neutralize the
XX CC function of NGF. Also described are: methods of treating a condition
XX CC caused by increased expression of NGF or increased sensitivity to NGF in
XX CC a patient; methods for detecting NGF in a biological sample; an NGF
XX CC specific binding agent comprising any of the 59 amino acid sequences
XX CC comprising, for e.g. 123, 107 or 14 amino acids, as mentioned in the
XX CC specification, and where the binding agent can bind to NGF; a
XX CC pharmaceutical composition comprising a pharmaceutical carrier and a
XX CC therapeutic amount of the antibody or binding agent cited above; or a
XX CC medicament for treating a painful disorder or condition associated with
XX CC increased expression of NGF or increased sensitivity to NGF, the
XX CC medicament comprising a pharmaceutical amount of a monoclonal antibody or
XX CC its immunologically functional immunoglobulin fragment, or pharmaceutical
XX CC salts of the monoclonal antibody or the fragment, where the monoclonal
XX CC antibody is at least one of the monoclonal antibody cited above, and a
XX CC pharmaceutical carrier, diluent or excipient; a nucleic acid molecule or
XX CC polynucleotide that encodes the above antibody or binding agent; an
XX CC isolated cell line that produces the above antibody or binding agent; an
XX CC expression vector comprising the above polynucleotide; and a host cell
XX CC comprising the nucleic acid or expression vector. The composition
XX CC (including the antibody) and methods are useful for manufacturing a
XX CC medicament for treating a painful disorder (e.g. acute pain, dental pain,
XX CC or pain from trauma or cancer), or a condition associated with increased
XX CC expression of NGF or increased sensitivity to NGF. This is the amino acid
XX CC sequence of a human NGF antibody light chain variable region.
XX SQ Sequence 107 AA;
Query Match 96.4%; Score 537; DB 9; Length 107;
Best Local Similarity 97.2%; Pred. No. 1.8e-34;
Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 DIQMTQSPSSLSASVGRVITTCRASQGISRLAWYQQKPKAPKSLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVITTCRASQGISRLAWYQQKPKAPKSLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDFTLISGLQPEDFATYICQYNSVPRTFGGQTKVEIK 107
Db 61 RFGSGSGTDFTLISGLQPEDFATYICQYNSVPRTFGGQTKVEIK 107
```

D6 61 RFGSGSGTDFTLTISLQPEDFATYYCQYNSYPWTFGGQTKVEIK 107

RESULT 10

AA872880
ID AA872880 standard; protein; 107 AA.

AC AA872880;

XX 10-MAY-2001 (first entry)

XX Human anti-HER2/neu antibody 3-F2 light chain.

XX Human; HER2; neu; erbB2; oncogene; cancer; antibody; immunotherapy; 3-F2;
KW 1-D2; 2-E8; growth factor receptor.

XX Homo sapiens.

XX WO200109187-A2.

XX 08-FEB-2001.

XX 25-JUL-2000; 2000WO-US020272.

XX 29-JUL-1999; 99US-0146313P.

XX 10-MAR-2000; 2000US-0188539P.

XX (MEDA-) MEDAREX INC.

XX Keler T, Deo Y;

XX WPI; 2001-168698/17.

XX N-PSDB; AAF75586.

XX New human monoclonal antibody that specifically binds to growth factor
PT receptor HER2/neu, for treating, preventing or diagnosing diseases
PT characterized by aberrant HER2/neu expression e.g. cancers.

XX Disclosure; Page 104-105; 113pp; English.

XX The present invention provides the protein and coding sequences for human
CC monoclonal antibodies which bind specifically to the HER2/neu growth
CC factor receptor (also known as erbB2). These are designated 3-F2, 1-D2
CC and 2-E8. They can be used in the immunotherapy-based treatment and
CC prognosis of cancers, particularly adenocarcinomas such as salivary
CC gland, stomach, kidney, mammary gland, lung and squamous cell carcinomas,
CC and ovarian cancer. The present sequence is part of an antibody of the
CC invention

XX Sequence 107 AA;

Query Match 96.1%; Score 535; DB 4; Length 107;
Best Local Similarity 96.3%; Pred. No. 2.6e-34;
Matches 103; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGISRLAWYQOKPEKAPKSLIYAASSLSQGVPS 60

DB 1 DIQMTQSPSSLSASVGRVTITCRASQGISRLAWYQOKPEKAPKSLIYAASSLSQGVPS 60

QY 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFGQTKVEIK 107

DB 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFGQTKLEIK 107

RESULT 11

ADO36490

ID ADO36490 standard; protein; 107 AA.

XX ADO36490;

XX 12-AUG-2004 (first entry)

XX Human anti-heparanase 2H8 vk amino acid sequence SEQ ID NO:4.

XX

human; monoclonal antibody; heparanase; heparanase inhibitor;
KW anti-heparanase antibody; cytostatic; immunosuppressive; antiarthritic;
KW antiasthmatic; antiinflammatory; dermatological; antiarteriosclerotic;
KW neuroprotective; nootropic; heparanase antagonist; cancer; tumour;
KW melanoma; lymphoma; prostate carcinoma; pancreatic carcinoma;
KW bladder carcinoma; fibrosarcoma; rhabdomyosarcoma; mastocytoma;
KW mammary adenocarcinoma; leukaemia; rheumatoid fibroblast;
KW autoimmune disease; arthritis; asthma; lupus erythematosus;
KW allograft rejection; vascular restenosis; atherosclerosis;
XX Alzheimer's disease.

XX Homo sapiens.

XX WO2004043989-A2.

XX 27-MAY-2004.

XX 05-NOV-2003; 2003WO-US035464.

XX 07-NOV-2002; 2002US-0424803P.

XX (MEDA-) MEDAREX INC.

XX (CELL-) CELLTech R & D.

XX Huang H, Holmes S, Mason S;

XX WPI; 2004-411694/38.

XX N-PSDB; ADO36489.

XX New human monoclonal antibody to heparanase, for use in treating or
PS preventing cancer, autoimmune disease, arthritis, asthma, lupus
PS erythematosus, allograft rejection, atherosclerosis, and Alzheimer's
PT disease.

XX Claim 47; SEQ ID NO 4; 108pp; English.

XX The present invention describes an isolated human monoclonal antibody
CC which binds to and inhibits activity of human heparanase. Human anti-
CC heparanase antibodies of the present invention have cytostatic,
CC immunosuppressive, antiarthritic, antiasthmatic, antiinflammatory,
CC dermatological, antiarteriosclerotic, neuroprotective and nootropic
CC activities, and can be used as heparanase antagonists. The antibody,
CC methods and compositions of the present invention are useful in treating
CC or preventing cancer or tumours, e.g. melanoma, lymphoma, prostate
CC carcinoma, pancreatic carcinoma, bladder carcinoma, fibrosarcoma,
CC rhabdomyosarcoma, mastocytoma, mammary adenocarcinoma, leukaemia or a
CC rheumatoid fibroblast, autoimmune disease, arthritis, asthma, lupus
CC erythematosus, allograft rejection, vascular restenosis, atherosclerosis,
CC and Alzheimer's disease. The present sequence represents a human anti-
CC heparanase 2H8 vk amino acid sequence, which is used in the
CC exemplification of the present invention.

XX Sequence 107 AA;

Query Match 96.1%; Score 535; DB 8; Length 107;
Best Local Similarity 96.3%; Pred. No. 2.6e-34;
Matches 103; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGISRLAWYQOKPEKAPKSLIYAASSLSQGVPS 60

DB 1 DIQMTQSPSSLSASVGRVTITCRASQGISRLAWYQOKPEKAPKSLIYAASSLSQGVPS 60

QY 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFGQTKVEIK 107

DB 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFGQTKLEIK 107

RESULT 12

ADO36502

ID ADO36502 standard; protein; 107 AA.

XX

AC ADO36502;

XX 12-AUG-2004 (first entry)
DT Human anti-heparanase 5G10 Vκ amino acid sequence SEQ ID NO:16.
DE
XX
KW human; monoclonal antibody; heparanase; heparanase inhibitor;
KW anti-heparanase antibody; cytostatic; immunosuppressive; antiarthritic;
KW antiasthmatic; antiinflammatory; dermatological; antiarteriosclerotic;
KW neuroprotective; nontropic; heparanase antagonist; cancer; tumour;
KW melanoma; lymphoma; prostate carcinoma; pancreatic carcinoma;
KW bladder carcinoma; fibrosarcoma; rhabdomyosarcoma; mastocytoma;
KW mammary adenocarcinoma; leukaemia; rheumatoid fibroblast;
KW autoimmune disease; arthritis; asthma; lupus erythematosus;
KW allograft rejection; vascular restenosis; atherosclerosis;
KW Alzheimer's disease.
XX
OS Homo sapiens.
XX
XX WO2004043989-A2.
PN
XX 27-MAY-2004.
PD
XX 05-NOV-2003; 2003WO-US035464.
XX
XX 07-NOV-2002; 2002US-0424803P.
XX
XX (MEDA-) MEDAREX INC.
PA (CELL-) CELLTech R & D.
XX
XX Huang H, Holmes S, Mason S;
PI
XX WPI; 2004-411694/38.
XX
XX N-PSDB; ADO36493.
DR
XX
XX New human monoclonal antibody to heparanase, for use in treating or
PT preventing cancer, autoimmune disease, arthritis, asthma, lupus
PT erythematosus, allograft rejection, atherosclerosis, and Alzheimer's
PT disease.
XX
XX Claim 47; SEQ ID NO 16; 108pp; English.
XX
XX The present invention describes an isolated human monoclonal antibody
CC which binds to and inhibits activity of human heparanase. Human anti-
CC heparanase antibodies of the present invention have cytostatic,
CC immunosuppressive, antiarthritic, antiasthmatic, antiinflammatory,
CC dermatological, antiarteriosclerotic, neuroprotective and nontropic
CC activities, and can be used as heparanase antagonists. The antibody,
CC methods and compositions of the present invention are useful in treating
CC or preventing cancer or tumours, e.g. melanoma, lymphoma, prostate
CC carcinoma, pancreatic carcinoma, bladder carcinoma, fibrosarcoma,
CC rhabdomyosarcoma, mastocytoma, mammary adenocarcinoma, leukaemia or a
CC rheumatoid fibroblast, autoimmune disease, arthritis, asthma, lupus
CC erythematosus, allograft rejection, vascular restenosis, atherosclerosis,
CC and Alzheimer's disease. The present sequence represents a human anti-
CC heparanase 5G10 Vκ amino acid sequence, which is used in the
CC exemplification of the present invention.
XX
XX Sequence 107 AA;
Query Match 96.1%; Score 535; DB 8; Length 107;
Best Local Similarity 96.3%; Pred. No. 2.6e-34;
Matches 103; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAAYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAAYQOKPEKAPKSLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFGQTKVEIK 107
Db 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFGQTKVEIK 107
RESULT 13

ADO36494
ID ADO36494 standard; protein; 107 AA.
XX
AC ADO36494;
XX
XX 12-AUG-2004 (first entry)
DT
XX Human anti-heparanase 22D9 Vκ amino acid sequence SEQ ID NO:8.
DE
XX human; monoclonal antibody; heparanase; heparanase inhibitor;
KW anti-heparanase antibody; cytostatic; immunosuppressive; antiarthritic;
KW antiasthmatic; antiinflammatory; dermatological; antiarteriosclerotic;
KW neuroprotective; nontropic; heparanase antagonist; cancer; tumour;
KW melanoma; lymphoma; prostate carcinoma; pancreatic carcinoma;
KW bladder carcinoma; fibrosarcoma; rhabdomyosarcoma; mastocytoma;
KW mammary adenocarcinoma; leukaemia; rheumatoid fibroblast;
KW autoimmune disease; arthritis; asthma; lupus erythematosus;
KW allograft rejection; vascular restenosis; atherosclerosis;
KW Alzheimer's disease.
XX
OS Homo sapiens.
XX
XX WO2004043989-A2.
PN
XX 27-MAY-2004.
PD
XX 05-NOV-2003; 2003WO-US035464.
XX
XX 07-NOV-2002; 2002US-0424803P.
XX
XX (MEDA-) MEDAREX INC.
PA (CELL-) CELLTech R & D.
XX
XX Huang H, Holmes S, Mason S;
PI
XX WPI; 2004-411694/38.
XX
XX N-PSDB; ADO36493.
DR
XX
XX New human monoclonal antibody to heparanase, for use in treating or
PT preventing cancer, autoimmune disease, arthritis, asthma, lupus
PT erythematosus, allograft rejection, atherosclerosis, and Alzheimer's
PT disease.
XX
XX Claim 11; SEQ ID NO 8; 108pp; English.
XX
XX The present invention describes an isolated human monoclonal antibody
CC which binds to and inhibits activity of human heparanase. Human anti-
CC heparanase antibodies of the present invention have cytostatic,
CC immunosuppressive, antiarthritic, antiasthmatic, antiinflammatory,
CC dermatological, antiarteriosclerotic, neuroprotective and nontropic
CC activities, and can be used as heparanase antagonists. The antibody,
CC methods and compositions of the present invention are useful in treating
CC or preventing cancer or tumours, e.g. melanoma, lymphoma, prostate
CC carcinoma, pancreatic carcinoma, bladder carcinoma, fibrosarcoma,
CC rhabdomyosarcoma, mastocytoma, mammary adenocarcinoma, leukaemia or a
CC rheumatoid fibroblast, autoimmune disease, arthritis, asthma, lupus
CC erythematosus, allograft rejection, vascular restenosis, atherosclerosis,
CC and Alzheimer's disease. The present sequence represents a human anti-
CC heparanase 22D9 Vκ amino acid sequence, which is used in the
CC exemplification of the present invention.
XX
XX Sequence 107 AA;
Query Match 96.1%; Score 535; DB 8; Length 107;
Best Local Similarity 96.3%; Pred. No. 2.6e-34;
Matches 103; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAAYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAAYQOKPEKAPKSLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFGQTKVEIK 107

Dd 61 RFGSGSGTDFTLTISSLPEDFATYYCQYNSYPYTFGGQTKLEIK 107

RESULT 14

AEBA48576
ID AEB48576 standard; protein; 234 AA.

XX AC AEB48576;

XX DT 06-OCT-2005 (first entry)

XX DE Human kappa light chain-TAKA signal peptide fusion protein.

XX KW monoclonal antibody; antibody production; light chain; alpha amylase;

XX KW TAKA; fusion protein.

XX OS Homo sapiens.

XX OS Aspergillus oryzae.

XX FN WO2005070962-A1.

XX PD 04-AUG-2005.

XX PF 20-JAN-2005; 2005WO-DK000035.

XX PR 21-JAN-2004; 2004DK-00000077.

XX PR 05-FEB-2004; 2004DK-00000174.

XX PR 12-MAY-2004; 2004DK-00000761.

XX PA (NOVO) NOVOZYMES AS.

XX PI Lehmbeck J, Wahlbom F;

XX DR WPI; 2005-533997/54.

XX PT Producing a monoclonal antibody by providing a heterokaryon fungus comprising a first nucleus and a second nucleus and culturing the heterokaryon fungus for expression of antibody light and heavy chains.

XX PS Example 9; SEQ ID NO 25; 94pp; English.

XX CC The invention describes a method of producing a monoclonal antibody comprising providing a heterokaryon fungus comprising a first nucleus comprising a sequence encoding a light chain of an antibody, and a second nucleus comprising a sequence encoding a heavy chain of an antibody, and culturing the heterokaryon fungus for expression of the antibody light and heavy chains. Also described are: a nucleic acid construct comprising a first nucleic acid sequence encoding a light chain of an antibody and a third nucleic acid sequence encoding a signal peptide heterologous to the first nucleic acid sequence; a nucleic acid construct comprising a first nucleic acid sequence encoding a heavy chain of an antibody and a third nucleic acid sequence encoding a signal peptide heterologous to the first nucleic acid sequence; a nucleic acid construct comprising a first nucleic acid sequence encoding a light chain of an antibody and a second nucleic acid sequence encoding a light chain of an antibody and a second nucleic acid sequence encoding a cellulose binding domain; a nucleic acid construct comprising a first nucleic acid sequence encoding a heavy chain of an antibody and a second nucleic acid sequence encoding a cellulose binding domain; a heterokaryon fungal host cell comprising a first nucleus and a second nucleus, where the first nucleus comprises a first nucleic acid construct comprising a first nucleic acid sequence encoding a light chain of an antibody, and the second nucleus comprises a second nucleic acid construct comprising a first nucleic acid sequence encoding a heavy chain of an antibody, and where at least one of the nucleic acid constructs further comprises a second nucleic acid sequence encoding a polypeptide or a functional part normally secreted by a fungus; and a heterokaryon fungal host cell comprising a first nucleus and a second nucleus, where the first nucleus comprises a first nucleic acid construct comprising a first nucleic acid sequence encoding a light chain of an antibody, and the second nucleus comprises a second nucleic acid construct comprising a first nucleic acid sequence encoding a heavy chain of an antibody, and where at least one of the nucleic acid constructs further comprises a third nucleic acid sequence encoding a signal peptide heterologous to the first nucleic acid sequence. The method is useful for

CC producing monoclonal antibodies in heterokaryon fungus or in fungal host cells. This is the amino acid sequence of a fusion protein comprising human kappa light chain in which the native signal sequence has been replaced with the alpha amylase (TAKA) signal peptide.

XX SQ Sequence 234 AA;

Query Match 96.1%; Score 535; DB 9; Length 234;
Best Local Similarity 96.3%; Pred. No. 5.4e-34;
Matches 103; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60
|||||
Db 21 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 80
|||||

Qy 61 RFGSGSGTDFTLTISSLPEDFATYYCQYNSYPYTFGGQTKVEIK 107
|||||

Db 81 RFGSGSGTDFTLTISSLPEDFATYYCQYNSYPYTFGGQTKLEIK 127
|||||

RESULT 15

ADV86270

ID ADV86270 standard; protein; 236 AA.

XX AC ADV86270;

XX DT 24-FEB-2005 (first entry)

XX DE Anti-human CTGF monoclonal antibody mAb1 light chain protein.

XX KW antibody engineering; immunotherapy; antibody;

XX KW connective tissue growth factor; immunoglobulin; hypertension;

XX KW hypotensive; cardiovascular disease; hyperglycemia; antidiabetic;

XX KW diabetes; metabolic disorder; endocrine disorder;

XX KW congestive heart failure; arthritis; antiarthritic; inflammation;

XX KW antiinflammatory; cancer; cytostatic; neoplasm.

XX OS Homo sapiens.

XX FN US2004248206-A1.

XX PD 09-DEC-2004.

XX PF 01-JUN-2004; 2004US-00858186.

XX PR 04-JUN-2003; 2003US-0475598P.

XX PA (LINA/) LIN A Y.

XX PA (NEFF/) NEFF T B.

XX PA (OLIV/) OLIVER N A.

XX PA (USIN/) USINGER W R.

XX PA (WANG/) WANG Q.

XX PA (YEOW/) YEOWELL D A.

XX PI Lin AY, Neff TB, Oliver NA, Usinger WR, Wang Q, Yeowell DA;

XX WPI; 2005-072821/08.

XX DR N-PSDB; ADV86269.

XX Novel isolated antibody specifically binding to connective tissue growth factor (CTGF), useful for neutralizing activity associated with CTGF and treating CTGF-associated disorder such as hypertension, hyperglycemia or diabetes.

XX Claim 32; SEQ ID NO 20; 54pp; English.

XX CC The invention relates to an isolated antibody or its fragment that specifically binds to connective tissue growth factor (CTGF) polypeptide having at least a portion of sequence of 62 amino acids fully defined in specification, or of an orthologous polypeptide derived from non-human species, having immunoglobulin sequence of 469 or 236 amino acids fully defined in specification, or antibody produced by cell line identified by ATCC accession number PTA-6006. (I) is useful for neutralizing an

CC activity associated with CTGF, which involves contacting (I) with a CTGF
 CC polypeptide in vitro or in vivo in a subject, under conditions suitable
 CC for formation of a complex comprising the antibody and the CTGF
 CC polypeptide, thus neutralizing the activity associated with CTGF. The
 CC subject has hypertension, hyperglycemia, diabetes, congestive heart
 CC failure, arthritis, and local or systemic inflammation. The subject has
 CC or is at risk for having a CTGF-associated disorder such as cancer. The
 CC cancer is chosen from acute lymphoblastic leukemia, dermatofibromas,
 CC breast cancer, breast carcinoma desmoplasia, angiolipoma, angioleiomyoma,
 CC desmoplastic cancer, prostate cancer, ovarian cancer, colorectal cancer,
 CC pancreatic cancer, gastrointestinal cancer, and liver cancer. The CTGF-
 CC associated disorder is a fibrotic disorder chosen from idiopathic
 CC pulmonary fibrosis, kidney fibrosis, glomerular sclerosis, ocular
 CC fibrosis, osteoarthritis, scleroderma, cardiac fibrosis, or liver
 CC fibrosis. (I) is useful for treating or preventing a CTGF-associated
 CC disorder in a subject having or at risk for having the disorder, which
 CC involves administering (I) to the subject. The subject is at risk due to
 CC a condition chosen from hypertension, hyperglycemia, diabetes, myocardial
 CC infarction, arthritis, and inflammation. The CTGF-associated disorder is
 CC chosen from diabetic nephropathy, diabetic retinopathy, and diabetic
 CC cardiovascular disease, or cancer. (II) is useful for treating CTGF-
 CC associated disorders (claimed). (I) is useful for quantitatively and
 CC qualitatively detecting CTGF in a sample, diagnosing disease or disorder
 CC associated with CTGF, identifying whether or not an individual has a
 CC predisposition to develop a CTGF-associated disorder, and for monitoring
 CC the therapeutic efficacy of treatment of a CTGF-associated disorder, and
 CC also as affinity purification agents. This sequence corresponds to the
 CC anti-human CTGF protein monoclonal antibody light chain protein.
 XX

SQ Sequence 236 AA;

Query Match 96.1%; Score 535; DB 9; Length 236;
 Best Local Similarity 96.3%; Pred. No. 5.5e-34;
 Matches 103; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
 Db 23 DIQMTQSPSSLSASVGRVTITCRASQGISRLAWYQOKPEKAPKSLIYAASSLSQGVPS 82
 Qy 61 RFGSGSGGTDFLTISGLQPEDFATYYCQYNSYPRTFGQGTKEIK 107
 Db 83 RFGSGSGGTDFLTISGLQPEDFATYYCQYNSYPRTFGQGTKEIK 129

Search completed: December 3, 2005, 14:25:03
 Job time : 184.992 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 14:11:59 ; Search time 29.2612 Seconds
(without alignments)
351.837 Million cell updates/sec

Title: US-10-769-144-8
Perfect score: 557
Sequence: 1 DIQMTQSPSSLSASVGRVT.....COQNSYPRTFGQTKVEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	500	89.8	125	2 S40333	Ig kappa chain V-J
2	496	89.0	107	2 T69017	anti-HIV1 envelope
3	491	88.2	129	2 S40369	Ig kappa chain - h
4	489	87.8	131	2 S40352	Ig kappa chain V-J
5	486	87.3	117	2 S46376	Ig kappa chain V-J
6	485	87.1	123	2 S40331	Ig kappa chain - h
7	484	86.9	117	2 B21056	Ig kappa chain pre
8	483	86.7	128	2 S46372	Ig light chain var
9	480	86.2	117	2 S46371	Ig kappa chain V-J
10	480	86.2	125	2 S40353	Ig kappa chain V-J
11	479	86.0	117	1 K1HU11	Ig kappa chain pre
12	479	86.0	123	2 S40313	Ig kappa chain V-J
13	479	86.0	125	2 S40349	Ig kappa chain V-J
14	478	85.8	132	2 S38646	Ig kappa chain V-I
15	476	85.5	108	1 K1HU6L	Ig kappa chain V-I
16	476	85.5	141	2 A49134	Ig kappa chain V-I
17	474.5	85.2	107	2 S47183	Ig kappa chain - h
18	474.5	85.2	124	2 S40336	Ig kappa chain V-I
19	474	85.1	108	1 K1HUEN	Ig kappa chain V-I
20	474	85.1	127	2 S11240	Ig kappa chain V-I
21	473	84.9	132	2 S40334	Ig kappa chain - h
22	472.5	84.8	107	2 S36275	Ig kappa chain V-I
23	472	84.7	107	2 S36264	Ig kappa chain V-I
24	471	84.6	108	2 B49047	Ig kappa chain V-I
25	471	84.6	127	2 S40367	Ig kappa chain V-J
26	469	84.2	124	2 S40318	Ig kappa chain - h
27	469	84.2	125	2 S40316	Ig kappa chain V-I
28	468	84.0	108	1 K1HU6U	Ig kappa chain V-I
29	467	83.8	108	1 K1HU6U	Ig kappa chain V-I

30	466	83.7	108	2 S36277	Ig lambda chain V
31	466	83.7	122	2 S40370	Ig kappa chain - h
32	465	83.5	108	1 K1HUWE	Ig kappa chain V-I
33	465	83.5	108	2 S36279	Ig lambda chain V
34	465	83.5	117	2 C21056	Ig kappa chain pre
35	465	83.5	130	2 S40368	Ig kappa chain - h
36	462	82.9	108	2 S19674	Ig kappa chain V-I
37	461.5	82.9	108	2 S30521	Ig kappa chain V-I
38	461	82.8	107	2 S36262	Ig lambda chain V
39	460	82.6	107	2 S36269	Ig lambda chain V
40	459	82.4	108	1 K1HUHU	Ig kappa chain V-I
41	458	82.2	110	2 PNO535	Ig kappa chain V-I
42	457.5	82.1	107	1 K1HUAR	Ig kappa chain V-I
43	457.5	82.1	108	2 S34007	Ig kappa chain V-I
44	457	82.0	105	2 S36266	Ig lambda chain V
45	456	81.9	108	1 K1HUAG	Ig kappa chain V-I

ALIGNMENTS

RESULT 1

S40333
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40333
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40333
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-125 <KLE>
A;Cross-references: UNIPARC:UPI0000116153; EMBL:X72443; NID:g441354; PIDN:CAAS1111.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;34-108/Domain: immunoglobulin homology <IMM>

Query Match 89.8%; Score 500; DB 2; Length 125;
Best Local Similarity 89.7%; Pred. No. 1.4e-36;
Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy	1	DIQMTQSPSSLSASVGRVTITCRASQISGSIWLAWYQQKPEKAPKSLIYAASSLQSGVPS 60
Db	19	DIQMTQSPSTLSASVGRVTITCRASQISGSIWLAWYQQKPEKAPKSLIYKASSLESQVPS 78
Qy	61	RFGSGSGTDTLTISGLQPEDFATYYCQQNSYPRTFGQTKVEIK 107
Db	79	RFGSGSGTFTLTISLQPDFATYYCQQNSYPRTFGQTKVEIK 125

RESULT 2

T69017
anti-HIV1 envelope protein gp120 V3 loop monoclonal antibody L chain V region - human (F
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
C;Accession: T69017
R;Chin, L.T.; Duenas, M.; Levi, M.; Hinkula, J.; Wahren, B.; Borrebaeck, C.A.
Immunol. Lett. 44, 25-30, 1995
A;Title: Molecular characterization of a human anti-HIV 1 monoclonal antibody revealed a
A;Reference number: I54563; MUID:95237884; PMID:7721339
A;Accession: T69017
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-107 <RES>
A;Cross-references: UNIPARC:UPI0000113F9C; GB:S77140; NID:g913352; PIDN:AAB34102.1; PID:
C;Genetics:
A;Gene: Ig V kappa
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

```
Query Match      89.0%; Score 496; DB 2; Length 107;
Best Local Similarity 90.7%; Pred. No. 2.7e-38;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVITTCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 1 DIQWTQSPSSLSASVGRVITTCRASHDIGSYLAWYQOKPEKAPESLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTDTLTISGLQPEDFATYYCCQYNSYPRTFGGQTKVEIK 107
Db 61 RFGSGSGTDTLTISGLQPEDFATYYCCQYNSYPRTFGGQTKVLIK 107

RESULT 3
S40369
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40369
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40369
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-129 <KLE>
A/Cross-references: UNIPARC:UPI0000116177; EMBL:X72479; NID:9441426; PIDN:CAA51147.1; PII
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/37-111/Domain: immunoglobulin homology <IMM>

Query Match      88.2%; Score 491; DB 2; Length 129;
Best Local Similarity 89.7%; Pred. No. 9.2e-38;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVITTCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 22 DIQWTQSPSSLSASVGRVITTCRASVISHNLVWFQOKPKAPKSLIYAASSLSQGVPS 81

Qy 61 RFGSGSGTDTLTISGLQPEDFATYYCCQYNSYPRTFGGQTKVEIK 107
Db 82 KFGSGSGTDTLTISGLQPEDFATYYCCQYNSYPRTFGGQTKLEIK 128

RESULT 4
S40352
Ig kappa chain V-J-C region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40352
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40352
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-131 <KLE>
A/Cross-references: UNIPARC:UPI0000116166; EMBL:X72462; NID:9441392; PIDN:CAA51130.1; PII
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/36-110/Domain: immunoglobulin homology <IMM>

Query Match      87.8%; Score 489; DB 2; Length 131;
Best Local Similarity 88.8%; Pred. No. 1.4e-37;
Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVITTCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 21 DIQWTQSPSSLSASVGRVITTCRASQGISNLYAWYQOKPKVPLIYAASLTLSQGVPS 80

Qy 61 RFGSGSGTDTLTISGLQPEDFATYYCCQYNSYPRTFGGQTKVEIK 107
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Db 81 RFGSGSGTDTLTISGLQPEDVATYYCQYNSVPRTFGGQTKVEIK 127

RESULT 5
S46376
Ig kappa chain V-J region (T33-14) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C/Accession: S46376; S38649
R/Bensimon, C.; Chaatagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A/Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene re
A/Reference number: S46369; MUID:94313975; PMID:8039491
A/Accession: S46376
A/Molecule type: mRNA
A/Residues: 1-117 <BEN>
A/Cross-references: UNIPARC:UPI00001165A9; EMBL:Z27177; NID:9415969; PIDN:CAA81701.1; PII
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/25-99/Domain: immunoglobulin homology <IMM>

Query Match      87.3%; Score 486; DB 2; Length 117;
Best Local Similarity 87.9%; Pred. No. 2.4e-37;
Matches 94; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVITTCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 10 DIQWTQSPSSVSASIGRVITTCRASQDISSWLAWYQOKPKAPKLLIYAASSLSQGVPL 69

Qy 61 RFGSGSGTDTLTISGLQPEDFATYYCCQYNSYPRTFGGQTKVEIK 107
Db 70 RFGSGSGTDTLTISGLQPEDFATYYCCQANSFPRGFGPTKVDIK 116

RESULT 6
S40331
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40331
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40331
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-123 <KLE>
A/Cross-references: UNIPARC:UPI0000116151; EMBL:X72441; NID:9441350; PIDN:CAA51109.1; PII
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/32-106/Domain: immunoglobulin homology <IMM>

Query Match      87.1%; Score 485; DB 2; Length 123;
Best Local Similarity 90.7%; Pred. No. 3.1e-37;
Matches 97; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVITTCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 17 DIQWTQSPSSLSASVGRVITTCRASQISISYLAWYQOKPKAPKLLIYAASSLSQGVPS 76

Qy 61 RFGSGSGTDTLTISGLQPEDFATYYCCQYNSYPRTFGGQTKVEIK 107
Db 77 RFGSGSGTDTLTISGLQPEDFATYYCCQYSYTPRTPFGQTKVEIK 123

RESULT 7
B21056
Ig kappa chain precursor V region (HK134) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 21-Jan-2000
C/Accession: B21056
```

R;Bentley, D.L.; Rabbitts, T.H.
Cell 32, 181-189, 1983
A:Title: Evolution of immunoglobulin V genes: evidence indicating that recently duplicated
A:Reference number: A21056; MUID:83129397; PMID:6402305
A:Accession: B21056
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <BEN>
A:Cross-references: UNIPARC:UPI0000116772; GB:K01323; NID:g185995; PIDN:AAA58931.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;38-113/Domain: immunoglobulin homology <IMM>

Query Match 86.9%; Score 484; DB 2; Length 117;
Best Local Similarity 97.9%; Pred. No. 3.6e-37;
Matches 93; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60
Db 23 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 82

Qy 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYP 95
Db 83 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYP 117

RESULT 8
S46372
Ig light chain variable region (VJ) - human
C:Species: Homo sapiens (man)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S46372
R;Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene re
A:Reference number: S46369; MUID:94313975; PMID:8039491
A:Accession: S46372
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-128 <BEN>
A:Cross-references: UNIPARC:UPI0000176CA4; EMBL:227173
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 86.7%; Score 483; DB 2; Length 128;
Best Local Similarity 89.6%; Pred. No. 4.8e-37;
Matches 95; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 2 IQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPSR 61
Db 22 IRTITQSPSSLSASTGDRVTITCRASQGISRWLAWYQOKPGKAPKLLIYAASLTLSQSGVPSR 81

Qy 62 FSGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFGQGTKEIK 107
Db 82 FSGSGSGTDFTLTISGLQSEDATYYCQYNSYPRTFGQGTKEIK 127

RESULT 9
S46371
Ig kappa chain V-J region (T24-3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C:Accession: S46371; S38645
R;Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene re
A:Reference number: S46369; MUID:94313975; PMID:8039491
A:Accession: S46371
A:Molecule type: mRNA
A:Residues: 1-117 <BEN>
A:Cross-references: UNIPARC:UPI00001165A4; EMBL:227172; NID:g415959; PIDN:CAA81696.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F;23-97/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 480; DB 2; Length 117;
Best Local Similarity 85.3%; Pred. No. 8.3e-37;
Matches 93; Conservative 7; Mismatches 7; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60
Db 8 DIQMTQSPSTLSASVGDRTVITCRASRSISTWLAWYQOKPGKAPKLLIYKASTLESQSGVPS 67

Qy 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSY--PRTFQGTKEIK 107
Db 68 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYFPYTFQGTKEIK 116

RESULT 10
S40353
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40353
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40353
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLE>
A:Cross-references: UNIPARC:UPI0000176CAE; EMBL:X72463
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;30-104/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 480; DB 2; Length 125;
Best Local Similarity 87.9%; Pred. No. 8.9e-37;
Matches 94; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60
Db 15 DIQMTQSPSSLSASVGDRTVITCRASQIGNDLQWYQOKPGKAPKRLIYAASSFSQSGVPS 74

Qy 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFQGTKEIK 107
Db 75 RFGSGSGTDFTLTISGLQPEDFATYYCLOHNSYFLTFGGGTKEIK 121

RESULT 11
K1HUI1
Ig kappa chain precursor V-I region (HK101) - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1981 #sequence_revision 31-Mar-1981 #text_change 09-Jul-2004
C:Accession: A01881; A21056
R;Bentley, D.L.; Rabbitts, T.H.
Nature 288, 730-733, 1980
A:Title: Human immunoglobulin variable region genes - DNA sequences of two V-kappa genes
A:Reference number: A93241; MUID:81098966; PMID:6779204
A:Accession: A01881
A:Molecule type: DNA
A:Residues: 1-117 <BEN1>
A:Cross-references: UNIPROT:P01601; UNIPARC:UPI000012E144; GB:V00558; GB:J00244; GB:J002
A:Note: the sequence was determined from the germline gene
R;Bentley, D.L.; Rabbitts, T.H.
Cell 32, 181-189, 1983
A:Title: Evolution of immunoglobulin V genes: evidence indicating that recently duplicat
A:Reference number: A21056; MUID:83129397; PMID:6402305
A:Accession: A21056
A:Molecule type: DNA
A:Residues: 1-117 <BEN2>
A:Cross-references: UNIPARC:UPI000012E144; GB:K01322; NID:g185993; PIDN:AAA58930.1; PID
C:Genetics:
A:Gene: GDB:IGKV1

A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
A;Introns: 19/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-117/Product: Ig kappa chain V-I region (HK101) #status predicted <MAT>
F;38-112/Domain: immunoglobulin homology <IMM>
F;45-110/Disulfide bonds: #status predicted

Query Match 86.0%; Score 479; DB 1; Length 117;
Best Local Similarity 96.8%; Pred. No. 1e-36; Mismatches 0; Indels 0; Gaps 0;
Matches 92; Conservative 0

Qy 1 DIQNTQSPSSLSASVGRVITTCRASQGISRWLAAYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 23 DIQNTQSPSSLSASVGRVITTCRASQGISRWLAAYQOKPEKAPKSLIYAASSLSQGVPS 82

Qy 61 RFGSGSGTDFTLTISGLQPEDPATYCCQYNSYP 95
Db 83 RFGSGSGTDFTLTISGLQPEDPATYCCQYNSYP 117

RESULT 12
S40313
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40313
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40313
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-123 <KLE>
A;Cross-references: UNIPARC:UPI000011613F; EMBL:X72423; NID:9441314; PIDN:CAAS1091.1; PI10-769-144-8
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;32-106/Domain: immunoglobulin homology <IMM>

Query Match 86.0%; Score 479; DB 2; Length 123;
Best Local Similarity 87.9%; Pred. No. 1.e-36;
Matches 94; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQNTQSPSSLSASVGRVITTCRASQGISRWLAAYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 17 DIQNTQSPSSLSASVGRVITTCRASQGISRWLAAYQOKPEKAPKSLIYAASSLSQGVPS 76

Qy 61 RFGSGSGTDFTLTISGLQPEDPATYCCQYNSYPRTFGQGTKEIK 107
Db 77 RFGSGSGTDFTLTISGLQPEDPATYCCQYNSYPRTFGQGTKEIK 123

RESULT 13
S40349
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S40349
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40349
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-125 <KLE>
A;Cross-references: UNIPARC:UPI0000116163; EMBL:X72459; NID:9441386; PIDN:CAAS1127.1; PI10-769-144-8
C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>

Query Match 86.0%; Score 479; DB 2; Length 125;
Best Local Similarity 88.7%; Pred. No. 1.e-36;
Matches 94; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 2 IQNTQSPSSLSASVGRVITTCRASQGISRWLAAYQOKPEKAPKSLIYAASSLSQGVPSR 61
Db 19 IQNTQSPSSLSASVGRVITTCRASQGISRWLAAYQOKPEKAPKSLIYAASSLSQGVPSR 78

Qy 62 FSGSGSGTDFTLTISGLQPEDPATYCCQYNSYPRTFGQGTKEIK 107
Db 79 FSGSGSGTDFTLTISGLQPEDPATYCCQYNSYPRTFGQGTKEIK 124

RESULT 14
S38646
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S38646
R;Bensimon, C.; Chastagner, P.; Zouali, M.
submitted to the EMBL Data Library, November 1993
A;Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.
A;Reference number: S38643
A;Accession: S38646
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-132 <BEN>
A;Cross-references: UNIPARC:UPI00001165A5; EMBL:Z27173; NID:9415961; PIDN:CAAS1697.1; PI10-769-144-8
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;40-114/Domain: immunoglobulin homology <IMM>

Query Match 85.8%; Score 478; DB 2; Length 132;
Best Local Similarity 88.7%; Pred. No. 1.e-36;
Matches 94; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 2 IQNTQSPSSLSASVGRVITTCRASQGISRWLAAYQOKPEKAPKSLIYAASSLSQGVPSR 61
Db 26 IRTAQSPSSLSASVGRVITTCRASQGISRWLAAYQOKPEKAPKSLIYAASSLSQGVPSR 85

Qy 62 FSGSGSGTDFTLTISGLQPEDPATYCCQYNSYPRTFGQGTKEIK 107
Db 86 FSGSGSGTDFTLTISGLQPEDPATYCCQYNSYPRTFGQGTKEIK 131

RESULT 15
X1HUGL
Ig kappa chain V-I region (Gal) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C;Accession: A01867
R;Laure, C.J.; Watanabe, S.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 354, 1503-1504, 1973
A;Title: The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal), I
A;Reference number: A01867; MUID:75059122; PMID:4215718
A;Accession: A01867
A;Molecule type: protein
A;Residues: 1-108 <LAU>
A;Cross-references: UNIPROT:P01599; UNIPARC:UPI0000012E142
A;Note: the C region of this chain has the Inv (3) marker
C;Comment: This chain was isolated from a Waldenström's macroglobulin.
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMM>

F:23-88/Disulfide bonds: #status predicted

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Query Match      85.5%; Score 476; DB 1; Length 108;
Best Local Similarity 86.9%; Pred. No. 1.8e-36;
Matches 93; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy      1 DIQMTQSPSSLSASVGDRTTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Db      1 DIQMTQSPSSLSASVGDRTTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60

Qy      61 RFSGSGGTDFLTITISGLQPEDFATYCCQYNSYPRTFGGTKVEIK 107
Db      61 RFSGSGGTDFLTITISGLQPEDFATYCCQYNSYPRTFGGTKVEIK 107
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Search completed: December 3, 2005, 14:33:32
Job time : 29.2612 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 13:24:58 ; Search time 45.4204 Seconds
(without alignments)
194.765 Million cell updates/sec

Title: US-10-769-144-8

Perfect score: 557

Sequence: 1 DIQWTSFSSLSASVGRVT.....CQQNSYPRTFGGTKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	529	95.0	108	2	US-09-920-262A-8
2	499	89.6	107	1	US-07-934-373C-18
3	499	89.6	107	2	US-08-437-642B-18
4	499	89.6	107	2	US-08-146-206C-18
5	499	89.6	107	2	US-09-648-067A-14
6	499	89.6	107	2	US-09-705-686-18
7	499	89.6	107	2	US-09-705-392A-18
8	499	89.6	107	2	US-09-705-398-18
9	499	89.6	107	2	US-09-602-812A-5
10	499	89.6	107	4	PCT-US93-07832-18
11	499	89.6	108	2	US-08-974-899-3
12	499	89.6	108	2	US-09-795-798-3
13	499	89.6	108	2	US-08-908-469-12
14	497	89.2	109	1	US-07-934-373C-3
15	497	89.2	109	2	US-08-437-642B-3
16	497	89.2	109	2	US-08-146-206C-3
17	497	89.2	109	2	US-09-705-686-3
18	497	89.2	109	2	US-09-705-392A-3
19	497	89.2	109	2	US-09-705-398-3
20	497	89.2	109	4	PCT-US93-07832-3
21	497	89.2	236	2	US-09-859-053-30
22	491	88.2	109	2	US-09-025-769B-28
23	491	88.2	109	2	US-09-025-769B-43
24	491	88.2	109	2	US-09-490-070A-28
25	491	88.2	109	2	US-09-490-070A-43
26	491	88.2	109	2	US-09-490-153-28
27	491	88.2	109	2	US-09-490-153-43

28	491	88.2	109	2	US-09-490-324-28
29	491	88.2	109	2	US-09-490-324-43
30	488	87.6	108	2	US-08-974-899-2
31	488	87.6	108	2	US-09-795-798-2
32	486	87.3	107	2	US-10-330-613A-18
33	484	86.9	107	2	US-08-599-226-1
34	484	86.9	107	2	US-09-125-098-1
35	484	86.9	107	2	US-09-540-018-1
36	484	86.9	117	2	US-09-042-353-48
37	484	86.9	117	2	US-08-758-417A-313
38	483	86.7	107	2	US-08-599-226-9
39	483	86.7	107	2	US-09-125-098-9
40	483	86.7	107	2	US-09-540-018-9
41	482	86.5	109	2	US-09-157-370-3
42	481.5	86.4	109	2	US-09-798-058-4
43	481	86.4	107	1	US-08-276-852-84
44	481	86.4	107	1	US-08-899-575-84
45	481	86.4	107	1	US-08-899-575-84

ALIGNMENTS

RESULT 1
US-09-920-262A-8
; Sequence 8, Application US/09920262A
; Patent No. 6902734
; GENERAL INFORMATION:
; APPLICANT: Shealy, David
; APPLICANT: Knight, David
; APPLICANT: Scallon, Bernie
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Peritt, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0248
; CURRENT APPLICATION NUMBER: US/09/920.262A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,827
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver 3.1
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-262A-8

Query Match	95.0%	Score 529;	DB 2;	Length 108;
Best Local Similarity	95.3%	Pred. No. 1.8e-44;		
Matches 102;	Conservative 1;	Mismatches 4;	Indels 0;	Gaps 0;
Qy	1	DIQWTSFSSLSASVGRVTITCRASQISRWLAWYQOKPEKAPKSLIYAASLSQGVPS	60	
Db	1	DIQWTSFSSLSASVGRVTITCRASQISRWLAWYQOKPEKAPKSLIYAASLSQGVPS	60	
Qy	61	RFSGSGSGTDTLTITSGLOPEDEATYCCQNSYPRTFGGTKVEIK	107	
Db	61	RFSGSGSGTDTLTITSGLOPEDEATYCCQNSYPRTFGGTKVEIK	107	

RESULT 2
US-07-934-373C-18
; Sequence 18, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.

```

; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934.373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-9881
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-07-934-373C-18
;
Query Match 89.6%; Score 499; DB 1; Length 107;
Best Local Similarity 91.6%; Pred. No. 1.5e-41;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQQTSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPKAPKSLIYAASSLSQSGVPS 60
Db 1 DIQQTSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPKAPKSLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFGGQTKVEIK 107
Db 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFGGQTKVEIK 107

RESULT 3
US-08-437-642B-18
; Sequence 18, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437.642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:

; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-9881
; TELEFAX: 650/952-9881
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-437-642B-18
;
Query Match 89.6%; Score 499; DB 2; Length 107;
Best Local Similarity 91.6%; Pred. No. 1.5e-41;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQQTSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPKAPKSLIYAASSLSQSGVPS 60
Db 1 DIQQTSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPKAPKSLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFGGQTKVEIK 107
Db 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFGGQTKVEIK 107

RESULT 4
US-08-146-206C-18
; Sequence 18, Application US/08146206C
; Patent No. 6407213
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146.206C
; FILING DATE: 17-No. 6407213-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
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; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-146-206C-18

Query Match      89.6%; Score 499; DB 2; Length 107;
Best Local Similarity 91.6%; Pred. No. 1.5e-41;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAHYQOKPEKAPKSLIYAASSLSQGVPS 60
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAHYQOKPEKAPKSLIYAASSLSQGVPS 60
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:

Qy 61 RFGSGSGTDFLTITISGLQPEDFATYYCQYNSYPRTFGGTKVEIK 107
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
Db 61 RFGSGSGTDFLTITISGLQPEDFATYYCQYNSLPTWTFGGTKVEIK 107
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:

RESULT 5
US-09-648-067A-14
; Sequence 14, Application US/09648067A
; Patent No. 6627196
; GENERAL INFORMATION:
; APPLICANT: Baughman, Sharon A.
; APPLICANT: Shak Steven
; TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P175R1
; CURRENT APPLICATION NUMBER: US/09/648,067A
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,018
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US 60/213,822
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 14
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VL consensus sequence
US-09-648-067A-14

Query Match      89.6%; Score 499; DB 2; Length 107;
Best Local Similarity 91.6%; Pred. No. 1.5e-41;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAHYQOKPEKAPKSLIYAASSLSQGVPS 60
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAHYQOKPEKAPKSLIYAASSLSQGVPS 60
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:

Qy 61 RFGSGSGTDFLTITISGLQPEDFATYYCQYNSYPRTFGGTKVEIK 107
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
Db 61 RFGSGSGTDFLTITISGLQPEDFATYYCQYNSLPTWTFGGTKVEIK 107
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:

RESULT 6
US-09-705-686-18
; Sequence 18, Application US/09705686
; Patent No. 6639055
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

Query Match      89.6%; Score 499; DB 2; Length 107;
Best Local Similarity 91.6%; Pred. No. 1.5e-41;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAHYQOKPEKAPKSLIYAASSLSQGVPS 60
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAHYQOKPEKAPKSLIYAASSLSQGVPS 60
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:

Qy 61 RFGSGSGTDFLTITISGLQPEDFATYYCQYNSYPRTFGGTKVEIK 107
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
Db 61 RFGSGSGTDFLTITISGLQPEDFATYYCQYNSLPTWTFGGTKVEIK 107
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-NO. 6639055-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-686-18

Query Match      89.6%; Score 499; DB 2; Length 107;
Best Local Similarity 91.6%; Pred. No. 1.5e-41;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAHYQOKPEKAPKSLIYAASSLSQGVPS 60
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAHYQOKPEKAPKSLIYAASSLSQGVPS 60
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:

Qy 61 RFGSGSGTDFLTITISGLQPEDFATYYCQYNSYPRTFGGTKVEIK 107
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
Db 61 RFGSGSGTDFLTITISGLQPEDFATYYCQYNSLPTWTFGGTKVEIK 107
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:

RESULT 7
US-09-705-392A-18
; Sequence 18, Application US/09705392A
; Patent No. 6719971
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,392A
FILING DATE: 02-NO. 6719971-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
```

NAME: Lee, Wendy M.	REGISTRATION NUMBER: 40,378	REFERENCE/DOCKET NUMBER: P0709PID1 REVISED	TELECOMMUNICATION INFORMATION:	TELEPHONE: 650/225-1994	TELEFAX: 650/952-9881	INFORMATION FOR SEQ ID NO: 18:	SEQUENCE CHARACTERISTICS:	LENGTH: 107 amino acids	TYPE: Amino Acid	TOPOLOGY: Linear	SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-398-18											
Query Match 89.6%; Score 499; DB 2; Length 107;											
Best Local Similarity 91.6%; Pred. No. 1.5e-41;											
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;											
QY	1	DIQMTQSPSSLSASVGDRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS	60								
DB	1	DIQMTQSPSSLSASVGDRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS	60								
QY	61	RFSGSGSGTDFLTITISGLQPEDFATYYCOQYNSYPRTFQGGTKVEIK	107								
DB	61	RFSGSGSGTDFLTITISGLQPEDFATYYCOQYNSYPRTFQGGTKVEIK	107								
RESULT 8											
US-09-705-398-18											
Query Match 89.6%; Score 499; DB 2; Length 107;											
Best Local Similarity 91.6%; Pred. No. 1.5e-41;											
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;											
GENERAL INFORMATION:											
APPLICANT: Carter, Paul J.											
TITLE OF INVENTION: Method for Making Humanized Antibodies											
NUMBER OF SEQUENCES: 26											
CORRESPONDENCE ADDRESS:											
ADDRESSEE: Genentech, Inc.											
STREET: 1 DNA Way											
CITY: South San Francisco											
STATE: California											
COUNTRY: USA											
ZIP: 94080											
COMPUTER READABLE FORM:											
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk											
COMPUTER: IBM PC compatible											
OPERATING SYSTEM: PC-DOS/MS-DOS											
SOFTWARE: WinPatIn (Genentech)											
CURRENT APPLICATION DATA:											
APPLICATION NUMBER: US/09/705,398											
FILING DATE: 02-No. 6800738-2000											
CLASSIFICATION: <Unknown>											
PRIOR APPLICATION DATA:											
APPLICATION NUMBER: 08/146206											
FILING DATE: 17-NOV-1993											
APPLICATION NUMBER: 07/715272											
FILING DATE: 14-JUN-1991											
ATTORNEY/AGENT INFORMATION:											
NAME: Lee, Wendy M.											
REGISTRATION NUMBER: 40,378											
REFERENCE/DOCKET NUMBER: P0709PID2											
TELECOMMUNICATION INFORMATION:											
TELEPHONE: 650/225-1994											
TELEFAX: 650/952-9881											
INFORMATION FOR SEQ ID NO: 18:											
SEQUENCE CHARACTERISTICS:											
LENGTH: 107 amino acids											
TYPE: Amino Acid											
TOPOLOGY: Linear											
SEQUENCE DESCRIPTION: SEQ ID NO: 18:											
US-09-705-398-18											
Query Match 89.6%; Score 499; DB 2; Length 107;											
Best Local Similarity 91.6%; Pred. No. 1.5e-41;											
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;											
QY	1	DIQMTQSPSSLSASVGDRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS	60								
DB	1	DIQMTQSPSSLSASVGDRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS	60								
QY	61	RFSGSGSGTDFLTITISGLQPEDFATYYCOQYNSYPRTFQGGTKVEIK	107								
DB	61	RFSGSGSGTDFLTITISGLQPEDFATYYCOQYNSYPRTFQGGTKVEIK	107								
RESULT 9											
US-09-602-812A-5											
Query Match 89.6%; Score 499; DB 2; Length 107;											
Best Local Similarity 91.6%; Pred. No. 1.5e-41;											
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;											
GENERAL INFORMATION:											
APPLICANT: Adams, Camellia W.											
PATENT NO. 6949245											
APPLICANT: Presta, Leonard G.											
APPLICANT: Sliwkowski, Mark X.											
TITLE OF INVENTION: Humanized Anti-ErbB2 Antibodies and Treatment with											
TITLE OF INVENTION: Anti-ErbB2 Antibodies											
FILE REFERENCE: P1467R2											
CURRENT APPLICATION NUMBER: US/09/602,812A											
CURRENT FILING DATE: 2000-06-23											
PRIOR APPLICATION NUMBER: US 60/141,316											
PRIOR FILING DATE: 1999-06-25											
NUMBER OF SEQ ID NOS: 13											
SEQ ID NO 5											
LENGTH: 107											
TYPE: PRT											
ORGANISM: Artificial sequence											
FEATURE:											
OTHER INFORMATION: light chain consensus sequence											
US-09-602-812A-5											
Query Match 89.6%; Score 499; DB 2; Length 107;											
Best Local Similarity 91.6%; Pred. No. 1.5e-41;											
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;											
QY	1	DIQMTQSPSSLSASVGDRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS	60								
DB	1	DIQMTQSPSSLSASVGDRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS	60								
QY	61	RFSGSGSGTDFLTITISGLQPEDFATYYCOQYNSYPRTFQGGTKVEIK	107								
DB	61	RFSGSGSGTDFLTITISGLQPEDFATYYCOQYNSYPRTFQGGTKVEIK	107								
RESULT 10											
PCT-US93-07832-18											
Sequence 18, Application PC/TUS9307832											
GENERAL INFORMATION:											
APPLICANT: Genentech, Inc.											
TITLE OF INVENTION: Immunoglobulin Variants											
NUMBER OF SEQUENCES: 40											
CORRESPONDENCE ADDRESS:											
ADDRESSEE: Genentech, Inc.											
STREET: 460 Point San Bruno Blvd											
CITY: South San Francisco											

RESULT 13

US-08-908-469-12
; Sequence 12, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/225-9881
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-08-908-469-12
Query Match 89.6%; Score 499; DB 2; Length 108;
Best Local Similarity 91.6%; Pred. No. 1.5e-41;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 1 DIQWTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDFTLTISLQPEDFATYCCQYNSYPRTFGGTKVEIK 107
Db 61 RFGSGSGTDFTLTISLQPEDFATYCCQYNSLPTWTFGGTKVEIK 107

RESULT 14

US-07-934-373C-3
; Sequence 3, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco

; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-AUG-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-07-934-373C-3

Query Match 89.2%; Score 497; DB 1; Length 109;
Best Local Similarity 90.7%; Pred. No. 2.4e-41;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 1 DIQWTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDFTLTISLQPEDFATYCCQYNSYPRTFGGTKVEIK 107
Db 61 RFGSGSGTDFTLTISLQPEDFATYCCQYNSLPTWTFGGTKVEIK 107

RESULT 15

US-08-437-642B-3
; Sequence 3, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-437-642B-3

Query Match      89.2%; Score 497; DB 2; Length 109;
Best Local Similarity 90.7%; Pred. No. 2.4e-41;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQDVSSILAWYQOKPEKAPKLLIYAASSLESQVPS 60

Qy 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFGQGTKVEIK 107
Db 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSLPLYTFGQGTKVEIK 107

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 13:24:58 ; Search time 49.2408 Seconds
(without alignments)
194.765 Million cell updates/sec

Title: US-10-769-144-4

Perfect score: 621

Sequence: 1 EVQLVQSGAEVKKPGESLR.....TRGDRGVDMGQGLTVTVSS 116

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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- 2: /cgn2_6/ptodata/1/iaa/6 COMB.pdp.*
- 3: /cgn2_6/ptodata/1/iaa/H COMB.pdp.*
- 4: /cgn2_6/ptodata/1/iaa/PCRTUS COMB.pdp.*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pdp.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	556	89.5	120	2	US-09-025-769B-40 Sequence 40, Appl
2	556	89.5	120	2	US-09-025-769B-67 Sequence 67, Appl
3	556	89.5	120	2	US-09-025-769B-40 Sequence 40, Appl
4	556	89.5	120	2	US-09-490-070A-40 Sequence 40, Appl
5	556	89.5	120	2	US-09-490-070A-67 Sequence 67, Appl
6	556	89.5	120	2	US-09-490-153-40 Sequence 40, Appl
7	556	89.5	120	2	US-09-490-153-67 Sequence 67, Appl
8	556	89.5	120	2	US-09-490-324-40 Sequence 40, Appl
9	553.5	89.1	119	2	US-09-025-769B-26 Sequence 26, Appl
10	553.5	89.1	119	2	US-09-490-070A-26 Sequence 26, Appl
11	553.5	89.1	119	2	US-09-490-153-26 Sequence 26, Appl
12	553.5	89.1	119	2	US-09-490-324-26 Sequence 26, Appl
13	505.5	81.4	119	2	US-09-920-262A-7 Sequence 7, Appl
14	496.5	80.0	129	1	US-08-665-202-32 Sequence 32, Appl
15	496.5	80.0	129	2	US-09-315-574-32 Sequence 32, Appl
16	496.5	80.0	258	1	US-08-665-202-5 Sequence 5, Appl
17	496.5	80.0	258	2	US-09-315-574-5 Sequence 5, Appl
18	496.5	80.0	262	2	US-09-069-821-4 Sequence 4, Appl
19	496.5	80.0	262	2	US-09-956-086-4 Sequence 4, Appl
20	496.5	80.0	262	2	US-09-956-087-4 Sequence 4, Appl
21	496.5	80.0	282	2	US-09-420-592A-7 Sequence 7, Appl
22	496.5	80.0	282	2	US-09-985-442-7 Sequence 7, Appl
23	496.5	80.0	282	2	US-09-983-580-7 Sequence 7, Appl
24	495	79.7	98	1	US-08-665-202-33 Sequence 33, Appl
25	495	79.7	98	2	US-09-315-574-33 Sequence 33, Appl
26	495	79.7	98	2	US-10-194-975-45 Sequence 45, Appl
27	495	79.7	117	2	US-08-545-809A-133 Sequence 133, Appl

Sequence 133, Appl
Sequence 171, Appl
Sequence 171, Appl
Sequence 81, Appl
Sequence 81, Appl
Sequence 56, Appl
Sequence 56, Appl
Sequence 59, Appl
Sequence 59, Appl
Sequence 53, Appl
Sequence 54, Appl
Sequence 54, Appl
Sequence 54, Appl
Sequence 46, Appl
Sequence 46, Appl
Sequence 48, Appl
Sequence 55, Appl
Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-09-025-769B-40
; Sequence 40, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Pluckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-40

Query Match 89.5%; Score 556; DB 2; Length 120;
Best Local Similarity 89.2%; Pred. No. 1e-48;
Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDPTFTYWGVRMPGKGLNWGIIYPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDPTFTYWGVRMPGKGLNWGIIYPGDSDTIY 60
Qy 61 SPSPGQGVTTISADKSIISTAYLQWSLKASDTAMYCTR---GDRGVDMYQGQGLTIVTSS 116
Db 61 SPSPGQGVTTISADKSIISTAYLQWSLKASDTAMYCARWGQDGFYANDYMQGGLTIVTSS 120

RESULT 2

US-09-025-769B-67
; Sequence 67, Application US/09025769B
; Patent No. 630064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/S
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-025-769B-67

Query Match 89.5%; Score 556; DB 2; Length 120;
Best Local Similarity 89.2%; Pred. No. 1e-48;
Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDPTFTYWGVRMPGKGLNWGIIYPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDPTFTYWGVRMPGKGLNWGIIYPGDSDTIY 60
Qy 61 SPSPGQGVTTISADKSIISTAYLQWSLKASDTAMYCTR---GDRGVDMYQGQGLTIVTSS 116
Db 61 SPSPGQGVTTISADKSIISTAYLQWSLKASDTAMYCARWGQDGFYANDYMQGGLTIVTSS 120

RESULT 3

US-09-490-070A-40
; Sequence 40, Application US/09490070A
; Patent No. 6696248

GENERAL INFORMATION:

APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:

ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe

STREET: 1666 K Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Colin G. Sandercock, Esq.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 912-2000

TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 40:

US-09-490-070A-40

Query Match 89.5%; Score 556; DB 2; Length 120;
Best Local Similarity 89.2%; Pred. No. 1e-48;
Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDPTFTYWGVRMPGKGLNWGIIYPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDPTFTYWGVRMPGKGLNWGIIYPGDSDTIY 60
Qy 61 SPSPGQGVTTISADKSIISTAYLQWSLKASDTAMYCTR---GDRGVDMYQGQGLTIVTSS 116
Db 61 SPSPGQGVTTISADKSIISTAYLQWSLKASDTAMYCARWGQDGFYANDYMQGGLTIVTSS 120

RESULT 4

US-09-490-070A-67

; Sequence 67, Application US/09490070A

; Patent No. 6696248

; GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Pack, Peter

Ilag, Vic

Ge, Liming

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman

```

; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
;   APPLICANT: US/09/025,769B
;   FILING DATE: 18-FEB-1998
;   APPLICATION NUMBER: EP 95 11 3021.0
;   FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
;   NAME: James F. Haley, Jr., Esq.
;   REGISTRATION NUMBER: 27,794
;   REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212)596-9000
;   TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 40:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 120 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-490-153-40

Query Match      89.5%; Score 556; DB 2; Length 120;
Best Local Similarity 89.8%; Pred. No. 1e-48;
Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1

QY      1 EVLVVSGAEVKKPESLRISCKSGDSFTYYIGWVRQMPGKLEWGIYPGDSDTIY 60
DB      1 EVLVVSGAEVKKPESLRISCKSGDSFTYYIGWVRQMPGKLEWGIYPGDSDTIY 60
QY      61 SPFSFQGVITISADKSIATYLOWSSLKASDTAMYCYCTR----GDRGVYDWGGTLVTVSS 116
DB      61 SPFSFQGVITISADKSIATYLOWSSLKASDTAMYCARWGGDGFYAMDYWGQGLVTVSS 120

RESULT 6
US-09-490-153-67
; Sequence 67, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
;   APPLICANT: Knappik, Achim
;   PACK, Peter
;   ILIAG, Vic
;   GE, Liming
;   MORONEY, Simon
;   PLUECKTHUN, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;   STREET: 1251 Avenue of the Americas
;   CITY: New York
;   STATE: New York
;   COUNTRY: USA
;   ZIP: 10021
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/490,153
;   FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/025,769B
;   FILING DATE: 18-FEB-1998
;   APPLICATION NUMBER: EP 95 11 3021.0
;   FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
;   NAME: James F. Haley, Jr., Esq.
;   REGISTRATION NUMBER: 27,794
;   REFERENCE/DOCKET NUMBER: MORPHO/5

```

```

;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-490-153-67

Query Match      89.5%; Score 556; DB 2; Length 120;
Best Local Similarity 89.2%; Pred. No. 1e-48;
Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

Qy 1 EVQLVQSGAEVKPGESLRISCKGSGDFTTYTWIGVWRQMPGKGLWNGIIYPGDSDTIY 60
   |||||
Db 1 EVQLVQSGAEVKPGESLRISCKGSGDFTTYTWIGVWRQMPGKGLWNGIIYPGDSDTIY 60
   |||||

Qy 61 SPSPQGGVTTISADKSIISTAYLQWSSLSKASDTAMYCYCTR-----GDRGVYDYGQGTIVTVSS 116
   |||||
Db 61 SPSPQGGVTTISADKSIISTAYLQWSSLSKASDTAMYCYCARWGDDGFYANDYMGQGTIVTVSS 120
   |||||

RESULT 7
US-09-490-324-40
; Sequence 40, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:

US-09-490-324-40

Query Match      89.5%; Score 556; DB 2; Length 120;
Best Local Similarity 89.2%; Pred. No. 1e-48;
Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

Qy 1 EVQLVQSGAEVKPGESLRISCKGSGDFTTYTWIGVWRQMPGKGLWNGIIYPGDSDTIY 60
   |||||
Db 1 EVQLVQSGAEVKPGESLRISCKGSGDFTTYTWIGVWRQMPGKGLWNGIIYPGDSDTIY 60
   |||||

Qy 61 SPSPQGGVTTISADKSIISTAYLQWSSLSKASDTAMYCYCTR-----GDRGVYDYGQGTIVTVSS 116
   |||||
Db 61 SPSPQGGVTTISADKSIISTAYLQWSSLSKASDTAMYCYCARWGDDGFYANDYMGQGTIVTVSS 120
   |||||

RESULT 8
US-09-490-324-67
; Sequence 67, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-490-324-67

Query Match      89.5%; Score 556; DB 2; Length 120;
Best Local Similarity 89.2%; Pred. No. 1e-48;
Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

Qy 1 EVQLVQSGAEVKPGESLRISCKGSGDFTTYTWIGVWRQMPGKGLWNGIIYPGDSDTIY 60
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Db 1 EVQLVQSGAEVKPGESLRISCKGSGDFTTYTWIGVWRQMPGKGLWNGIIYPGDSDTIY 60
   |||||

Qy 61 SPSPQGGVTTISADKSIISTAYLQWSSLSKASDTAMYCYCTR-----GDRGVYDYGQGTIVTVSS 116
   |||||
Db 61 SPSPQGGVTTISADKSIISTAYLQWSSLSKASDTAMYCYCARWGDDGFYANDYMGQGTIVTVSS 120
   |||||
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
FILING DATE: 24-Jan-2000
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-153-26

Query Match 89.1%; Score 553.5; DB 2; Length 119;
Best Local Similarity 89.9%; Pred. No. 1.9e-48;
Matches 107; Conservative 2; Mismatches 7; Indels 3; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLWNGIYPGDSITY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLWNGIYPGDSITY 60

Qy 61 SPSPQGGVTTISADKSIISTAYLQNSLSKASDTAMYCYCTR---GDRGVYWGQGLTVTVSS 116
Db 61 SPSPQGGVTTISADKSIISTAYLQNSLSKASDTAMYCYCARLGGGGYFYDWGQGLTVTVSS 119

RESULT 12
US-09-490-324-26
Sequence 26, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769

FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-324-26

Query Match 89.1%; Score 553.5; DB 2; Length 119;
Best Local Similarity 89.9%; Pred. No. 1.9e-48;
Matches 107; Conservative 2; Mismatches 7; Indels 3; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLWNGIYPGDSITY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLWNGIYPGDSITY 60

Qy 61 SPSPQGGVTTISADKSIISTAYLQNSLSKASDTAMYCYCTR---GDRGVYWGQGLTVTVSS 116
Db 61 SPSPQGGVTTISADKSIISTAYLQNSLSKASDTAMYCYCARLGGGGYFYDWGQGLTVTVSS 119

RESULT 13
US-09-920-262A-7
Sequence 7, Application US/09920262A
Patent No. 6902734
GENERAL INFORMATION:
APPLICANT: Shealy, David
Knight, David
Scallion, Bernie
Giles-Komar, Jill
Perritt, David
TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
FILE REFERENCE: CEN0248
CURRENT APPLICATION NUMBER: US/09/920,262A
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 60/223,358
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: 60/236,827
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent In Ver 3.1
SEQ ID NO 7
LENGTH: 119
TYPE: PRT
ORGANISM: Homo sapiens
US-09-920-262A-7

Query Match 81.4%; Score 505.5; DB 2; Length 119;
Best Local Similarity 80.7%; Pred. No. 1.3e-43;
Matches 96; Conservative 9; Mismatches 11; Indels 3; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLWNGIYPGDSITY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLDWIGMSPVDSIRY 60

Qy 61 SPSPQGGVTTISADKSIISTAYLQNSLSKASDTAMYCYCTR---GDRGVYWGQGLTVTVSS 116
Db 61 SPSPQGGVTTISADKSIISTAYLQNSLSKASDTAMYCYCARRRPGQGYFDWGGQGLTVTVSS 119

RESULT 14

US-08-665-202-32
; Sequence 32, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-665-202-32

Query Match 80.0%; Score 496.5; DB 1; Length 129;
Best Local Similarity 72.9%; Pred. No. 1.1e-42;
Matches 94; Conservative 12; Mismatches 10; Indels 13; Gaps 1;

Qy 1 EVLVQSGAEVKKPGESLRISCKGSDSFTTWIGWVROMPGKGLWGLIYPGSDTIY 60
Db 1 QVQLQSGAELKPKGESLRISCKGSDSFTSYIAWVROMPGKGLWGLIYPGSDTKY 60

Qy 61 SPSPGQVTTISADKSIATYQLQWSSLKASDTAMYCTRGDRG-----VDYWG 107
Db 61 SPSPGQVTTISVDKSVSTAYLQWSSLKPSDSAVYFCARHVDVGYCSSNCAKWPYFQHWG 120

Qy 108 QGTLTVSS 116
Db 121 QGTLTVSS 129

Search completed: December 3, 2005, 14:11:28
Job time : 50.2408 secs

RESULT 15
US-09-315-574-32
; Sequence 32, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens

NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-32

Query Match 80.0%; Score 496.5; DB 2; Length 129;
Best Local Similarity 72.9%; Pred. No. 1.1e-42;
Matches 94; Conservative 12; Mismatches 10; Indels 13; Gaps 1;

Qy 1 EVLVQSGAEVKKPGESLRISCKGSDSFTTWIGWVROMPGKGLWGLIYPGSDTIY 60
Db 1 QVQLQSGAELKPKGESLRISCKGSDSFTSYIAWVROMPGKGLWGLIYPGSDTKY 60

Qy 61 SPSPGQVTTISADKSIATYQLQWSSLKASDTAMYCTRGDRG-----VDYWG 107
Db 61 SPSPGQVTTISVDKSVSTAYLQWSSLKPSDSAVYFCARHVDVGYCSSNCAKWPYFQHWG 120

Qy 108 QGTLTVSS 116
Db 121 QGTLTVSS 129

Search completed: December 3, 2005, 14:11:28
Job time : 50.2408 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 14:10:00 ; Search time 8.55102 Seconds
(without alignments)
256.916 Million cell updates/sec

Title: US-10-769-144-13

Perfect score: 33

Sequence: 1 TYWIG 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	5	ADR46830	Adi46830 Human ant
2	33	100.0	5	ADR69905	Adi69905 Human IL-
3	33	100.0	5	ADY26777	Ady26777 Human ant
4	33	100.0	5	AEA18875	Aea18875 Amino aci
5	33	100.0	88	AAR22576	Aar22576 Heavy cha
6	33	100.0	109	ADI05782	Adi05782 Human mon
7	33	100.0	116	AAM48005	Aam48005 Human mon
8	33	100.0	116	ADR46821	Adi46821 Human ant
9	33	100.0	121	ADX02171	Adx02171 SARS coro
10	33	100.0	121	ADX02051	Adx02051 SARS coro
11	33	100.0	121	ADX02099	Adx02099 SARS coro
12	33	100.0	121	ADX02055	Adx02055 SARS coro
13	33	100.0	121	ADX02059	Adx02059 SARS coro
14	33	100.0	121	ADX02111	Adx02111 SARS coro
15	33	100.0	121	ADX02107	Adx02107 SARS coro
16	33	100.0	121	ADX02103	Adx02103 SARS coro
17	33	100.0	121	ADX02175	Adx02175 SARS coro
18	33	100.0	121	ADX02191	Adx02191 SARS coro
19	33	100.0	122	AAU02586	Aau02586 Anti-adip
20	33	100.0	125	ADY26764	Ady26764 Anti-NGF
21	33	100.0	130	ABP96715	Abp96715 Human ant
22	33	100.0	130	ADR69902	Adi69902 Human IL-
23	33	100.0	130	AEA18872	Aea18872 Amino aci
24	33	100.0	145	ABB65181	Abb65181 Drosophil

25	33	100.0	248	5	ABP43990	Abp43990 Human Bly
26	33	100.0	248	7	ADG94817	Adg94817 Single ch
27	33	100.0	253	9	ADX01988	Adx01988 SARS coro
28	33	100.0	254	9	ADX02018	Adx02018 SARS coro
29	33	100.0	254	9	ADX01958	Adx01958 SARS coro
30	33	100.0	254	9	ADX02020	Adx02020 SARS coro
31	33	100.0	254	9	ADX01960	Adx01960 SARS coro
32	33	100.0	254	9	ADX01962	Adx01962 SARS coro
33	33	100.0	254	9	ADX02028	Adx02028 SARS coro
34	33	100.0	254	9	ADX01984	Adx01984 SARS coro
35	33	100.0	255	9	ADX01986	Adx01986 SARS coro
36	33	100.0	255	9	ADX01982	Adx01982 SARS coro
37	33	100.0	373	6	ABUS4587	Abu54587 Human NOV
38	33	100.0	411	8	ADR46829	Adr46829 Human pB1
39	33	100.0	430	6	ADA34166	Ada34166 Acinetoba
40	33	100.0	468	8	ADR46819	Adr46819 Human ant
41	33	100.0	551	8	ADP64795	Adp64795 Nematode
42	33	100.0	613	8	ADR46827	Adr46827 Human bet
43	33	100.0	1627	8	ADN21185	Adn21185 Bacterial
44	32	97.0	78	7	ADC24839	Adc24839 Human bre
45	32	97.0	116	3	AAB51824	Aab51824 Gene 47 h

ALIGNMENTS

RESULT 1

ADR46830

ID ADR46830 standard; peptide; 5 AA.

XX AC ADR46830;

XX AC ADR46830;

DT 18-NOV-2004 (first entry)

XX DE Human antibody B11 heavy chain variable region CDR1 SEQ ID NO:13.

XX DE Human antibody B11 heavy chain variable region CDR1 SEQ ID NO:13.

XX DE Human antibody B11 heavy chain variable region CDR1 SEQ ID NO:13.

XX DE Human antibody B11 heavy chain variable region CDR1 SEQ ID NO:13.

XX DE Human antibody B11 heavy chain variable region CDR1 SEQ ID NO:13.

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XX DE Human antibody B11 heavy chain variable region CDR1 SEQ ID NO:13.

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XX DE Human antibody B11 heavy chain variable region CDR1 SEQ ID NO:13.

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XX DE Human antibody B11 heavy chain variable region CDR1 SEQ ID NO:13.

XX DE Human antibody B11 heavy chain variable region CDR1 SEQ ID NO:13.

XX DE Human antibody B11 heavy chain variable region CDR1 SEQ ID NO:13.

XX DE Human antibody B11 heavy chain variable region CDR1 SEQ ID NO:13.

XX DE Human antibody B11 heavy chain variable region CDR1 SEQ ID NO:13.

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XX DE Human antibody B11 heavy chain variable region CDR1 SEQ ID NO:13.

XX DE Human antibody B11 heavy chain variable region CDR1 SEQ ID NO:13.

XX DE Human antibody B11 heavy chain variable region CDR1 SEQ ID NO:13.

XX DE Human antibody B11 heavy chain variable region CDR1 SEQ ID NO:13.

XX DE Human antibody B11 heavy chain variable region CDR1 SEQ ID NO:13.

XX DE Human antibody B11 heavy chain variable region CDR1 SEQ ID NO:13.

XX DE Human antibody B11 heavy chain variable region CDR1 SEQ ID NO:13.

XX DE Human antibody B11 heavy chain variable region CDR1 SEQ ID NO:13.

XX DE Human antibody B11 heavy chain variable region CDR1 SEQ ID NO:13.

XX DE Human antibody B11 heavy chain variable region CDR1 SEQ ID NO:13.

XX DE Human antibody B11 heavy chain variable region CDR1 SEQ ID NO:13.

XX DE Human antibody B11 heavy chain variable region CDR1 SEQ ID NO:13.

of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also described: (1) a molecular conjugate comprising a human antibody heavy chain and a human antibody light chain, where either or both chains are linked to beta2-microglobulin; (2) a molecular conjugate comprising a human single chain antibody that binds to human APCs linked to beta2-microglobulin, where the conjugate comprises the 411 amino acid sequence of SEQ ID NO:12 (ADR46829); (3) a composition comprising any of the molecular conjugates as described above, and a carrier, optionally in combination with an adjuvant; (4) inducing or enhancing a T cell-mediated immune response, against beta2-microglobulin, comprising contacting any of the molecular conjugates presented to T cells in a manner which induces or enhances a T cell-mediated response against the antigen; (5) immunising a subject comprising administering any of the molecular conjugates described above, optionally in combination with an adjuvant, a cytokine which stimulates proliferation of dendritic cells and/or an immunostimulatory agent; and (6) inducing or enhancing a cytotoxic T cell response against an antigen, comprising forming a conjugate of the antigen and a monoclonal antibody which binds to APCs, and contacting the conjugate either in vivo or ex vivo with APCs such that the antigen is internalised, processed and presented to T cells in a manner which induces or enhances a cytotoxic T cell response against the antigen. The molecular conjugate has cytotoxic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic, virucide and antimalarial activities, and can be used as a CD8 agonist, and in vaccines. The methods and compositions of the present invention are useful for inducing a cytotoxic T cell response, and in particular for treating autoimmune disorders, cancers and infectious diseases by eliciting a potent antigen-specific cytotoxic T lymphocyte response, including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and herpes. The present sequence represents the human antibody B11 heavy chain variable region complementarity determining region 1 (CDR1) amino acid sequence, which is used in the exemplification of the present invention.

Sequence 5 AA;

Query Match 100.0%; Score 33; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYWIG 5
|
|
|
|
|
DB 1 TYWIG 5

RESULT 2

ADR69905
ID ADR69905 standard; peptide; 5 AA.

AC ADR69905;

DT 02-DEC-2004 (first entry)

XX Human IL-15 monoclonal antibody VH-region CDR1 SEQ ID NO:5.

XX monoclonal antibody; heavy chain variable region; interleukin-15; IL-15;
XX antiarthritic; ophthalmological; neuroprotective; nontropic;
XX gastrointestinal; hepatotropic; antiallergic; haemostatic;
XX dermatological; respiratory; cytostatic; immunosuppressive; vasotrophic;
XX gynaecological; antimicrobial; CDR.

OS Homo sapiens.

XX WO2004076620-A2.

XX 10-SEP-2004.

XX 25-FEB-2004; 2004WO-IB000484.

XX 26-FEB-2003; 2003US-00374932.

PR 05-MAR-2003; 2003US-00379741.

XX (GENM-) GENMAB AS.

XX Van De Winkel JGJ, Van Dijk MA, Schuurman J, Gerritsen AF;
PI Baadsgaard OMS, Petersen J;
XX WPI; 2004-653391/63.

PT New isolated human monoclonal antibody that specifically binds to human
IL-15, useful for diagnosing, preventing or treating lupus, ulcerative
colitis, allograft rejection and graft-versus-host disease.

XX Claim 1; SEQ ID NO 5; 116pp; English.

XX The invention relates to a novel isolated human monoclonal antibody which
specifically binds to human interleukin-15 (IL-15) comprising at least
one CDR sequence from a fully defined sequence of 5, 17, 8, 12, 7 or 8
amino acids (ADR69905-ADR69910, respectively), a sequence at least 90,
95, 98 or 99% homologous to the amino acid sequences, or their fragments,
which retain the ability to specifically bind to human IL-15. A
monoclonal antibody of the invention has antiarthritic, ophthalmological,
neuroprotective, nontropic, gastrointestinal, hepatotropic, antiallergic,
haemostatic, dermatological, respiratory, cytostatic, immunosuppressive,
vasotrophic, gynaecological, and antimicrobial activity. The methods and
compositions of the present invention are useful for the prevention
and/or treatment of conditions associated with aberrant expression or
activity of the IL-15, such as arthritis, connective tissue disorders,
ophthalmological disorders, neurological disorders, gastrointestinal and
hepatic disorders, allergic disorders, haematologic disorders, allergic
disorders, skin disorders, pulmonary disorders, malignancies,
transplantation-derived disorders, endocrinological disorders, vascular
disorders, gynaecological disorders and infectious diseases, including
ankylosing spondylitis, systemic lupus erythematosus, ulcerative colitis,
allograft rejection and graft-versus-host disease. The present sequence
represents CDR1 of the heavy chain variable (VH) region of a human IL-15
monoclonal antibody of the invention.

Sequence 5 AA;

Query Match 100.0%; Score 33; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYWIG 5
|
|
|
|
|
DB 1 TYWIG 5

RESULT 3

ADY26777

ID ADY26777 standard; protein; 5 AA.

XX ADY26777;

XX 19-MAY-2005 (first entry)

XX Human anti-NGF-antibody heavy chain CDR1 SEQ ID NO 92.

XX analgesic; gene therapy; antibody engineering; pharmaceutical; pain;
XX neurological disease; NGF; nerve growth factor; heavy chain; CDR1.

OS Homo sapiens.

XX WO2005019266-A2.

XX 03-MAR-2005.

XX 15-JUL-2004; 2004WO-US022876.

XX 15-JUL-2003; 2003US-0487431P.

XX (AMGE-) AMGEN INC.

XX Wild KD, Treanor JJS, Huang H, Inoue H, Zhang TJ, Martin F;

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DR WPI; 2005-202606/21.
XX
XX New human anti-nerve growth factor (NGF) neutralizing antibodies useful
PT for manufacturing a medicament for treating painful disorders (e.g. acute
PT pain) or conditions associated with increased expression or sensitivity
PT to NGF.
XX
XX Claim 36; SEQ ID NO 92; 190pp; English.
XX
XX The invention describes an isolated human antibody that interacts with or
CC binds specifically to human nerve growth factor (NGF) and neutralize the
CC function of NGF. Also described are: methods of treating a condition
CC caused by increased expression of NGF or increased sensitivity to NGF in
CC a patient; methods for detecting NGF in a biological sample; an NGF
CC specific binding agent comprising any of the 59 amino acid sequences
CC comprising, for e.g. 123, 107 or 14 amino acids, as mentioned in the
CC specification, and where the binding agent can bind to NGF; a
CC pharmaceutical composition comprising a pharmaceutical carrier and a
CC therapeutic amount of the antibody or binding agent cited above; or a
CC medicament for treating a painful disorder or condition associated with
CC increased expression of NGF or increased sensitivity to NGF, the
CC medicament comprising a pharmaceutical amount of a monoclonal antibody or
CC its immunologically functional immunoglobulin fragment, or pharmaceutical
CC salts of the monoclonal antibody or the fragment, where the monoclonal
CC antibody is at least one of the monoclonal antibody cited above, and a
CC pharmaceutical carrier, diluent or excipient; a nucleic acid molecule or
CC polynucleotide that encodes the above antibody or binding agent; an
CC isolated cell line that produces the above antibody or binding agent; an
CC expression vector comprising the above polynucleotide; and a host cell
CC comprising the nucleic acid or expression vector. The composition
CC (including the antibody) and methods are useful for manufacturing a
CC medicament for treating a painful disorder (e.g. acute pain, dental pain,
CC or pain from trauma or cancer), or a condition associated with increased
CC expression of NGF or increased sensitivity to NGF. This is the amino acid
CC sequence of a human NGF antibody heavy chain complementarity determining
CC region 1 (CDR1).
XX
XX Sequence 5 AA;
SQ
Query Match 100.0%; Score 33; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TYWIG 5
Db 1 TYWIG 5
|||
|||
RESULT 4
AEAl8875
ID AEAl8875 standard; peptide; 5 AA.
XX
XX AEAl8875;
AC
XX
XX 28-JUL-2005 (first entry)
DT
XX
XX Amino acid sequence of anti-IL-15 antibody CDR peptide #1.
DE
XX
XX monocyte; interleukin-15; IL-15; IL-15 antagonist; apoptosis; gout;
KW connective disorder; neuroprotective; antigout; inflammation;
KW musculoskeletal disease; gastrointestinal-gen.; muscular-gen.; cardiant;
KW antiallergic; immune disorder; respiratory-gen.; neoplasm; cytostatic;
KW endocrine-gen.; vasotropic; antiinflammatory; cardiovascular disease;
KW antianemic; antimicrobial; infection; osteopathic; neurological disease;
KW gastrointestinal disease; hepatic disease; allergy;
KW hematological disease; dermatological disease; pulmonary disease;
KW prostatic cancer; endocrine disease; vasculitis; infectious disease;
KW renal disease; muscle disease; cardiac disorder; circulatory disorder;
KW blood clotting disorder; bone disease;
KW complementarity determining region; CDR.
XX
XX Homo sapiens.
OS
XX

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PN WO2005044303-A1.
XX
XX 19-MAY-2005.
PD
XX 05-NOV-2004; 2004WO-IB003895.
PF
XX 06-NOV-2003; 2003US-0518552P.
XX
XX (GENM-) GENMAB AS.
PA
XX
XX Beurskens F, Schuurman J, Parren P, Petersen J, Baadsgaard ODM;
PI WPI; 2005-356210/36.
XX
XX Treating diseases involving monocytic activity (e.g. cancer,
PT neurological, hematological, cardiac or metabolic disorders) comprises
PT administering an interleukin-15 antagonist that induces apoptosis of
PT monocytes.
XX
XX Claim 27; SEQ ID NO 5; 38pp; English.
FS
XX
XX The specification describes a method of treating a disease involving
CC monocytic activity. The method comprises administering an interleukin-15
CC (IL-15) antagonist that induces apoptosis of monocytes. The antagonist is
CC an agent that binds to IL-15 or IL-15R (interleukin-15 receptor), e.g. an
CC antibody. The method is useful for treating disorders involving monocytic
CC activity, such as gout, connective disorders, neurological diseases,
CC gastrointestinal or hepatic diseases, allergies, hematological diseases,
CC dermatological diseases, pulmonary diseases, prostatic cancer, endocrine
CC diseases, vasculitis, infectious diseases, renal diseases, muscle
CC diseases, cardiac disorders, circulatory disorders, blood clotting
CC disorder, and bone diseases. AEAl8875-AEAl8880 represent complementarity
CC determining regions (CDRs) derived from an anti-IL-15 antibody. This
CC antibody may be used in the method of the invention.
XX
XX Sequence 5 AA;
SQ
Query Match 100.0%; Score 33; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TYWIG 5
Db 1 TYWIG 5
|||
|||
RESULT 5
AAR22576
ID AAR22576 standard; protein; 88 AA.
XX
XX AAR22576;
AC
XX
XX 23-SEP-2004 (revised)
DT
XX 21-MAY-1992 (first entry)
DT
XX
XX Heavy chain VH16.1 from lysozyme binding scFv fragment.
DE
XX
XX Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;
KW g3p; binding; adsorption; gene VIII; diverse repertoire;
KW specific binding pairs; replicable genetic display package; human.
XX
XX Homo sapiens.
OS
XX Unidentified.
XX
XX WO9201047-A.
PN
XX
XX 23-JAN-1992.
PD
XX
XX 10-JUL-1990; 90GB-00015198.
PF
XX
XX 10-JUL-1990; 90GB-00015198.
PR
XX 19-OCT-1990; 90GB-00022845.
PR
XX 12-NOV-1990; 90GB-00024503.
PR

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PR 06-MAR-1991; 91GB-00004744.
PR 15-MAY-1991; 91GB-00010549.
PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PA (MEDI-) MED RES COUNCIL.
XX
XX McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD;
XX
XX WPI; 1992-056862/07.
DR
XX
XX Producing members of specific binding pairs - by expression in
PT recombinant host cells with a secreting replicable genetic display
PT package.
XX
XX Disclosure; Page ?; 209pp; English.
XX
XX PCR was used to prepare a human scFv library from RNA from white blood
XX cells from an unimmunised donor. Heavy chains from IgG and IGM antibodies
XX were amplified separately. Four separate libraries were generated (IGG-K,
XX IGG-lambda, IGM-K and IGM-lambda). The purified scFv fragments were
XX ligated into the phagemid pHEX1 for expression on the surface of fd
XX bacteriophage as gene III fusions. The clones were then subjected to
XX affinity selection for binding to lysozyme by selection on tubes followed
XX by analysis by ELISA. 50 positive lysozyme binding clones were
XX identified, 95% being from the IGM library. The clones gave three
XX different BstNI restriction patterns, and at least 2 clones from each
XX pattern was sequenced. The sequences indicated the presence of 4 unique
XX human VH-VL combinations. The sequence shown here is one of the VH chains
XX found. See also AAR21260-307, 309-312, AAR22450, AAR22565, AAR22567-81
XX
XX Revised record issued on 23-SEP-2004 : Correction to sequence location
XX
XX Sequence 88 AA;
XX
XX Query Match 100.0%; Score 33; DB 2; Length 88;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TYWIG 5
XX |||||
XX 31 TYWIG 35
XX
XX
XX
XX RESULT 6
XX ADI05782
XX ID ADI05782 standard; protein; 109 AA.
XX
XX AC ADI05782;
XX
XX DT 22-APR-2004 (first entry)
XX
XX DE Human monoclonal antibody CM-2 variable region heavy chain, SEQ ID 12.
XX
XX KW Cytostatic; Gene therapy; neoplasm; antibody; variable region;
XX heavy chain; proliferative disorder; human; CM-2.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Region 16..22
XX FT /label= CDR1
XX FT Region 40..47
XX FT /label= CDR2
XX FT Region 86..100
XX FT /label= CDR3
XX
XX PN WO2004005351-A2.
XX
XX PD 15-JAN-2004.
XX
XX PP 02-JUL-2003; 2003WO-IB003487.
XX

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PR 04-JUL-2002; 2002DE-01029906.
PR 04-JUL-2002; 2002DE-01029907.
PR 06-JUL-2002; 2002DE-01030516.
XX
XX (ONCO-) ONCOMAB GMBH.
XX
XX Mueller-Hermelink H, Vollmers H;
XX
XX WPI; 2004-122575/12.
DR N-PSDB; ADI05781.
XX
XX New purified polypeptide (e.g. an antibody) that induces apoptosis of a
PT neoplastic cell, useful for diagnosing or treating a neoplasm or a
PT proliferative disorder in mammals, including humans.
XX
XX Claim 93; SEQ ID NO 12; 106pp; English.
XX
XX The present invention relates to neoplasm specific antibody variable
XX region light and heavy chain sequences (ADI05771-ADI05782) The antibody
XX sequences are useful in diagnosing or treating a neoplasm or a
XX proliferative disorder in a mammal.
XX
XX Sequence 109 AA;
XX
XX Query Match 100.0%; Score 33; DB 8; Length 109;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TYWIG 5
XX |||||
XX 20 TYWIG 24
XX
XX
XX RESULT 7
XX AAM48005
XX ID AAM48005 standard; protein; 116 AA.
XX
XX AC AAM48005;
XX
XX DT 08-MAR-2002 (first entry)
XX
XX DE Human monoclonal antibody B11 variable heavy chain protein.
XX
XX KW Human; monoclonal antibody; B11; antigen binding portion; dendritic cell;
XX mannose receptor; growth; cytolysis; pathogen; virus; bacterium;
XX autoimmune disease; inflammatory disorder; rheumatoid arthritis;
XX multiple sclerosis; diabetes mellitus; immunomodulatory;
XX antiinflammatory; antirheumatic; antiarthritic; neuroprotective;
XX antidiabetic; antianaemic; endocrine; dermatological; antithyroid;
XX uropathic; ophthalmological; muscular.
XX
XX OS Homo sapiens.
XX
XX PN WO200185798-A2.
XX
XX PD 15-NOV-2001.
XX
XX PF 08-MAY-2001; 2001WO-US015114.
XX
XX PR 08-MAY-2000; 2000US-0203126P.
XX 07-SEP-2000; 2000US-0230739P.
XX
XX (MEDA-) MEDAREX INC.
XX
XX Deo YM, Keler T;
XX
XX WPI; 2002-089788/12.
DR N-PSDB; ABA05500.
XX
XX New human monoclonal antibodies specific for dendritic cells, useful for
PT inhibiting growth or inducing cytolysis of a dendritic cell and treating
PT or preventing a dendritic cell mediated disease, e.g., autoimmune
PT disorders.
XX

```

XX PS Example 2; Fig 13; 95pp; English.

XX CC The invention relates to human monoclonal antibodies or their antigen

XX CC binding portions that specifically bind to dendritic cells and has one or

XX CC more of the following characteristics: (a) a binding affinity constant to

XX CC a dendritic cell of at least about 10 to the power 7 M-1; (b) the ability

XX CC to opsonise a dendritic cell; (c) the ability to internalise after

XX CC binding to dendritic cells; or (d) the ability to activate dendritic

XX CC cells. The isolated human monoclonal antibody or its antigen binding

XX CC portion may also have any of the following characteristics: (a) mediates

XX CC cytolysis of dendritic cells in the presence of human effector cells; or

XX CC (b) inhibits growth of dendritic cells. The antibodies or its antigen

XX CC binding portion, binds to and blocks the human mannose receptor on

XX CC dendritic cells. The antibodies have immunomodulatory, antiinflammatory,

XX CC antirheumatic, antiarthritic, neuroprotective, antidiabetic, antianaemic,

XX CC endocrine, dermatological, antithyroid, uropathic, ophthalmological and

XX CC muscular activity. The antibodies or their antigen-binding fragments are

XX CC useful for inhibiting growth of a dendritic cell, inducing cytolysis of a

XX CC dendritic cell, treating or preventing a dendritic cell mediated disease,

XX CC detecting the presence of a dendritic cell, targeting an antigen to a

XX CC dendritic cell and preventing binding of a pathogen (a virus or a

XX CC bacterium) to human mannose receptor on dendritic cells. In particular,

XX CC the antibodies may be used to treat, autoimmune disease, graft versus

XX CC host disease, immune system or inflammatory disorders (e.g. rheumatoid

XX CC arthritis), multiple sclerosis, diabetes mellitus, myasthenia gravis,

XX CC pernicious anaemia, Addison's disease, lupus erythematosus, Reiter's

XX CC syndrome and Graves disease. The present sequence is that of the human

XX CC monoclonal antibody B11 variable heavy chain, useful to the invention

XX SQ Sequence 116 AA;

Query Match 100.0%; Score 33; DB 5; Length 116;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0;

QY 1 TWIG 5
 |||||
 Db 31 TWIG 35

RESULT 8

AD46821
 ID AD46821 standard; protein; 116 AA.

XX AC AD46821;

XX DT 18-NOV-2004 (first entry)

XX DE Human antibody B11 heavy chain variable region protein SEQ ID NO:4.

XX KW molecular conjugate; monoclonal antibody; human antigen presenting cell;
 XX KW antigen presenting cell; APC; human; beta human chorionic gonadotropin;
 XX KW betahCG; beta chorionic gonadotropin; antibody;
 XX KW T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
 XX KW immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
 XX KW CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
 XX KW melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
 XX KW antibody B11; heavy chain variable region.

XX OS Homo sapiens.

XX PN WO2004074432-A2.

XX PD 02-SEP-2004.

XX PF 30-JAN-2004; 2004WO-US002725.

XX PR 31-JAN-2003; 2003US-0443979P.

XX PA (MEDA-) MEDAREX INC.

XX PI Keler T, Endres M, He L, Ramakrishna V;

XX WPI; 2004-635555/61.
 DR N-PSDB; AD46820.

XX PT New molecular conjugate having a monoclonal antibody that binds to human
 PT APCs linked to a beta human chorionic gonadotropin, useful for inducing a
 PT cytotoxic T cell response in cancers and infectious diseases.

XX Claim 11; SEQ ID NO 4; 82pp; English.

XX CC The present invention describes a molecular conjugate comprising a
 CC monoclonal antibody that binds to human antigen presenting cells (APCs)
 CC linked to beta human chorionic gonadotropin (betahCG), where the antibody
 CC comprises a heavy and/or light chain variable region derived from a human
 CC VH5-51 or Vk-L15 germline sequence with the 98 or 95 amino acid sequences
 CC of SEQ ID NO:30 or 32 (AD46847, or AD46849), respectively. Also
 CC described: (1) a molecular conjugate comprising a human antibody heavy
 CC chain and a human antibody light chain, where either or both chains are
 CC linked to betahCG; (2) a molecular conjugate comprising a human single
 CC chain antibody that binds to human APCs linked to betahCG, where the
 CC conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
 CC (AD46829); (3) a composition comprising any of the molecular conjugates
 CC as described above, and a carrier, optionally in combination with an
 CC adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
 CC against betahCG, comprising contacting any of the molecular conjugates
 CC described above with APCs such that the antigen is processed and
 CC presented to T cells in a manner which induces or enhances a T cell-
 CC mediated response against the antigen; (5) immunising a subject
 CC comprising administering any of the molecular conjugates described above,
 CC optionally in combination with an adjuvant, a cytokine which stimulates
 CC proliferation of dendritic cells and/or an immunostimulatory agent; and
 CC (6) inducing or enhancing a cytotoxic T cell response against an antigen,
 CC comprising forming a conjugate of the antigen and a monoclonal antibody
 CC which binds to APCs, and contacting the conjugate either in vivo or ex
 CC vivo with APCs such that the antigen is internalised, processed and
 CC presented to T cells in a manner which induces or enhances a cytotoxic T
 CC cell response against the antigen. The molecular conjugate has
 CC cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
 CC virucide and antimalarial activities, and can be used as a CD8 agonist,
 CC and in vaccines. The methods and compositions of the present invention
 CC are useful for inducing a cytotoxic T cell response, and in particular
 CC for treating autoimmune disorders, cancers and infectious diseases by
 CC eliciting a potent antigen-specific cytotoxic T lymphocyte response,
 CC including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
 CC herpes. The present sequence represents a human antibody B11 heavy chain
 CC variable region, which is used in the exemplification of the present
 CC invention.

XX SQ Sequence 116 AA;

Query Match 100.0%; Score 33; DB 8; Length 116;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0;

QY 1 TWIG 5
 |||||
 Db 31 TWIG 35

RESULT 9

ADX02171

XX ID ADX02171 standard; protein; 121 AA.

XX AC ADX02171;

XX DT 21-APR-2005 (first entry)

XX DE SARS coronavirus antibody heavy chain SEQ ID NO 427.

XX KW severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide;
 KW respiratory disease; infection; antibody; heavy chain.

XX OS SARS coronavirus.

PR 14-APR-2004; 2004WO-EP050516.
 PR 29-APR-2004; 2004WO-EP050643.
 XX (CRUC-) CRUCELL HOLLAND BV.
 XX Ter Meulen JH, De Kruif CA, Van Den Brink EN, Goudemits J;
 PI WPI; 2005-142879/15.
 DR N-PSDB; ADX02098.
 XX New binding molecules that specifically bind to severe acute respiratory
 PT syndrome (SARS)-coronavirus (CoV), useful for diagnosing, preventing or
 PT treating conditions resulting from SARS-CoV.
 XX Claim 4; SEQ ID NO 355; 633pp; English.
 XX The invention relates to a binding molecule, or its variant, capable of
 CC specifically binding to a severe acute respiratory syndrome (SARS)-
 CC coronavirus (CoV). The composition (including the binding molecule or its
 CC functional variant, or the immunoconjugate) is useful as a medicament for
 CC the diagnosis, prophylaxis or treatment of a condition resulting from a
 CC SARS-CoV, or in the preparation of the medicament. The present sequence
 CC represents a SARS coronavirus binding molecule heavy chain.
 XX SQ Sequence 121 AA;
 Query Match 100.0%; Score 33; DB 9; Length 121;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TYWIG 5
 Db |||||
 33 TYWIG 37

RESULT 12
 ADX02055
 ID ADX02055 standard; protein; 121 AA.
 AC ADX02055;
 XX 21-APR-2005. (first entry)
 XX SARS coronavirus antibody heavy chain SEQ ID NO 311.
 XX severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide;
 KW respiratory disease; infection; antibody; heavy chain.
 XX SARS coronavirus.
 OS WO2005012360-A2.
 XX 10-FEB-2005.
 XX 21-JUL-2004; 2004WO-EP051568.
 XX 22-JUL-2003; 2003WO-EP050328.
 PR 01-SEP-2003; 2003WO-EP050391.
 PR 16-OCT-2003; 2003WO-EP050723.
 PR 24-NOV-2003; 2003WO-EP050883.
 PR 04-DEC-2003; 2003WO-EP050943.
 PR 02-FEB-2004; 2004WO-EP050067.
 PR 13-FEB-2004; 2004WO-EP050127.
 PR 19-MAR-2004; 2004WO-EP050334.
 PR 07-APR-2004; 2004WO-EP050464.
 PR 14-APR-2004; 2004WO-EP050516.
 PR 29-APR-2004; 2004WO-EP050643.
 XX (CRUC-) CRUCELL HOLLAND BV.
 XX Ter Meulen JH, De Kruif CA, Van Den Brink EN, Goudemits J;
 PI WPI; 2005-142879/15.
 XX New binding molecules that specifically bind to severe acute respiratory
 PT syndrome (SARS)-coronavirus (CoV), useful for diagnosing, preventing or
 PT treating conditions resulting from SARS-CoV.
 XX Claim 4; SEQ ID NO 315; 633pp; English.

DR N-PSDB; ADX02054.
 XX New binding molecules that specifically bind to severe acute respiratory
 PT syndrome (SARS)-coronavirus (CoV), useful for diagnosing, preventing or
 PT treating conditions resulting from SARS-CoV.
 XX Claim 4; SEQ ID NO 311; 633pp; English.
 XX The invention relates to a binding molecule, or its variant, capable of
 CC specifically binding to a severe acute respiratory syndrome (SARS)-
 CC coronavirus (CoV). The composition (including the binding molecule or its
 CC functional variant, or the immunoconjugate) is useful as a medicament for
 CC the diagnosis, prophylaxis or treatment of a condition resulting from a
 CC SARS-CoV, or in the preparation of the medicament. The present sequence
 CC represents a SARS coronavirus binding molecule heavy chain.
 XX SQ Sequence 121 AA;
 Query Match 100.0%; Score 33; DB 9; Length 121;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TYWIG 5
 Db |||||
 33 TYWIG 37

RESULT 13
 ADX02059
 ID ADX02059 standard; protein; 121 AA.
 AC ADX02059;
 XX 21-APR-2005 (first entry)
 XX SARS coronavirus antibody heavy chain SEQ ID NO 315.
 XX severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide;
 KW respiratory disease; infection; antibody; heavy chain.
 XX SARS coronavirus.
 OS WO2005012360-A2.
 XX 10-FEB-2005.
 XX 21-JUL-2004; 2004WO-EP051568.
 XX 22-JUL-2003; 2003WO-EP050328.
 PR 01-SEP-2003; 2003WO-EP050391.
 PR 16-OCT-2003; 2003WO-EP050723.
 PR 24-NOV-2003; 2003WO-EP050883.
 PR 04-DEC-2003; 2003WO-EP050943.
 PR 02-FEB-2004; 2004WO-EP050067.
 PR 13-FEB-2004; 2004WO-EP050127.
 PR 19-MAR-2004; 2004WO-EP050334.
 PR 07-APR-2004; 2004WO-EP050464.
 PR 14-APR-2004; 2004WO-EP050516.
 PR 29-APR-2004; 2004WO-EP050643.
 XX (CRUC-) CRUCELL HOLLAND BV.
 XX Ter Meulen JH, De Kruif CA, Van Den Brink EN, Goudemits J;
 PI WPI; 2005-142879/15.
 DR N-PSDB; ADX02058.
 XX New binding molecules that specifically bind to severe acute respiratory
 PT syndrome (SARS)-coronavirus (CoV), useful for diagnosing, preventing or
 PT treating conditions resulting from SARS-CoV.
 XX Claim 4; SEQ ID NO 315; 633pp; English.

CC The invention relates to a binding molecule, or its variant, capable of
 CC specifically binding to a severe acute respiratory syndrome (SARS)-
 CC coronavirus (CoV). The composition (including the binding molecule or its
 CC functional variant, or the immunoconjugate) is useful as a medicament for
 CC the diagnosis, prophylaxis or treatment of a condition resulting from a
 CC SARS-CoV, or in the preparation of the medicament. The present sequence
 CC represents a SARS coronavirus binding molecule heavy chain.
 XX
 SQ Sequence 121 AA;

Query Match 100.0%; Score 33; DB 9; Length 121;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
 |||||
 Db 33 TYWIG 37

RESULT 14
 ADX02111
 ID ADX02111 standard; protein; 121 AA.

XX AC ADX02111;
 XX
 DT 21-APR-2005 (first entry)

DE SARS coronavirus antibody heavy chain SEQ ID NO 367.

XX severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide;
 KW respiratory disease; infection; antibody; heavy chain.
 XX

OS SARS coronavirus.
 XX
 PN WO2005012360-A2.

XX PD 10-FEB-2005.

XX PF 21-JUL-2004; 2004WO-EP051568.

XX PR 22-JUL-2003; 2003WO-EP050328.

XX PR 01-SEP-2003; 2003WO-EP050391.

XX PR 16-OCT-2003; 2003WO-EP050723.

XX PR 24-NOV-2003; 2003WO-EP050883.

XX PR 04-DEC-2003; 2003WO-EP050943.

XX PR 02-FEB-2004; 2004WO-EP050067.

XX PR 13-FEB-2004; 2004WO-EP050127.

XX PR 19-MAR-2004; 2004WO-EP050334.

XX PR 07-APR-2004; 2004WO-EP050464.

XX PR 14-APR-2004; 2004WO-EP050516.

XX PR 29-APR-2004; 2004WO-EP050643.

XX PA (CRUC-) CRUCELL HOLLAND BV.

XX PI Ter Meulen JH, De Kruif CA, Van Den Brink EN, Goudsmit J;

XX WPI; 2005-142879/15.

XX DR N-PSDB; ADX02110.

XX New binding molecules that specifically bind to severe acute respiratory

PT syndrome (SARS)-coronavirus (CoV), useful for diagnosing, preventing or

PT treating conditions resulting from SARS-CoV.

XX Claim 4; SEQ ID NO 367; 633pp; English.

XX The invention relates to a binding molecule, or its variant, capable of
 CC specifically binding to a severe acute respiratory syndrome (SARS)-
 CC coronavirus (CoV). The composition (including the binding molecule or its
 CC functional variant, or the immunoconjugate) is useful as a medicament for
 CC the diagnosis, prophylaxis or treatment of a condition resulting from a
 CC SARS-CoV, or in the preparation of the medicament. The present sequence
 CC represents a SARS coronavirus binding molecule heavy chain.
 XX

SQ Sequence 121 AA;

Query Match 100.0%; Score 33; DB 9; Length 121;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
 |||||
 Db 33 TYWIG 37

RESULT 15
 ADX02107
 ID ADX02107 standard; protein; 121 AA.

XX AC ADX02107;

XX DT 21-APR-2005 (first entry)

XX SARS coronavirus antibody heavy chain SEQ ID NO 363.

XX severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide;
 KW respiratory disease; infection; antibody; heavy chain.
 XX

OS SARS coronavirus.

XX PN WO2005012360-A2.

XX PD 10-FEB-2005.

XX PF 21-JUL-2004; 2004WO-EP051568.

XX PR 22-JUL-2003; 2003WO-EP050328.

XX PR 01-SEP-2003; 2003WO-EP050391.

XX PR 16-OCT-2003; 2003WO-EP050723.

XX PR 24-NOV-2003; 2003WO-EP050883.

XX PR 04-DEC-2003; 2003WO-EP050943.

XX PR 02-FEB-2004; 2004WO-EP050067.

XX PR 13-FEB-2004; 2004WO-EP050127.

XX PR 19-MAR-2004; 2004WO-EP050334.

XX PR 07-APR-2004; 2004WO-EP050464.

XX PR 14-APR-2004; 2004WO-EP050516.

XX PR 29-APR-2004; 2004WO-EP050643.

XX PA (CRUC-) CRUCELL HOLLAND BV.

XX PI Ter Meulen JH, De Kruif CA, Van Den Brink EN, Goudsmit J;

XX WPI; 2005-142879/15.

XX DR N-PSDB; ADX02106.

XX New binding molecules that specifically bind to severe acute respiratory

PT syndrome (SARS)-coronavirus (CoV), useful for diagnosing, preventing or

PT treating conditions resulting from SARS-CoV.

XX Claim 4; SEQ ID NO 363; 633pp; English.

XX The invention relates to a binding molecule, or its variant, capable of
 CC specifically binding to a severe acute respiratory syndrome (SARS)-
 CC coronavirus (CoV). The composition (including the binding molecule or its
 CC functional variant, or the immunoconjugate) is useful as a medicament for
 CC the diagnosis, prophylaxis or treatment of a condition resulting from a
 CC SARS-CoV, or in the preparation of the medicament. The present sequence
 CC represents a SARS coronavirus binding molecule heavy chain.
 XX

SQ Sequence 121 AA;

Query Match 100.0%; Score 33; DB 9; Length 121;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
 |||||

Db 33 TYWIG 37

Search completed: December 3, 2005, 14:25:04
Job time : 9.55102 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 14:11:59 ; Search time 1.36735 Seconds
(without alignments)
351.837 Million cell updates/sec

Title: US-10-769-144-13

Perfect score: 33

Sequence: 1 TYWIG 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

P1R 80:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	98	2 PH0877	Ig heavy chain V r
2	33	100.0	102	2 PH1260	Ig heavy chain V r
3	33	100.0	102	2 PH1263	Ig heavy chain V r
4	33	100.0	117	2 S19669	Ig heavy chain V r
5	33	100.0	119	2 S36257	Ig heavy chain V r
6	33	100.0	123	2 PH1413	Ig heavy chain V r
7	33	100.0	127	2 PH1409	Ig heavy chain V r
8	33	100.0	175	2 S57903	probable amino aci
9	33	100.0	181	2 F75561	hypothetical prote
10	33	100.0	324	2 E84505	hypothetical prote
11	33	100.0	332	2 E71105	hypothetical prote
12	33	100.0	333	2 G75055	hypothetical prote
13	33	100.0	348	2 E82896	hemin permease U03
14	33	100.0	390	2 D82186	beta-lactamase-rel
15	33	100.0	466	2 A95963	probable oxidoredu
16	33	100.0	539	2 S30871	hypothetical prote
17	33	100.0	539	2 A88546	protein R107.1 (im
18	33	100.0	1562	2 T43022	ATP-binding multidi
19	32	97.0	156	2 S67248	hypothetical prote
20	32	97.0	281	2 S55646	hypothetical prote
21	32	97.0	294	2 AC1905	ABC transporter su
22	32	97.0	387	2 T22841	hypothetical prote
23	32	97.0	528	2 S50563	hypothetical prote
24	32	97.0	533	1 GR5YCP	cytosine/purine tr
25	32	97.0	760	2 E81808	hypothetical prote
26	32	97.0	881	2 E87387	TonB-dependent rec
27	32	97.0	1077	2 D90387	peptidase related
28	32	97.0	1118	1 A49724	protein-tyrosine-p
29	31	93.9	69	2 AB1333	hypothetical prote

30 31 93.9 69 2 AB1704 hypothetical prote
31 31 93.9 83 2 E83178 30S ribosomal prot
32 31 93.9 100 1 F70309 protein export mem
33 31 93.9 301 2 H97505 probable nikC prot
34 31 93.9 301 2 AD2724 ABC transporter, m
35 31 93.9 372 2 T42426 conserved hypothet
36 31 93.9 384 2 G84482 hypothetical prote
37 31 93.9 384 2 T49128 hypothetical prote
38 31 93.9 535 2 E87656 hypothetical prote
39 31 93.9 641 2 S63645 NADH2 dehydrogenas
40 29 87.9 78 2 F69750 conserved hypothet
41 29 87.9 86 2 S12580 Ig heavy chain V r
42 29 87.9 98 2 PH1274 Ig heavy chain V r
43 29 87.9 98 2 S26907 Ig heavy chain V r
44 29 87.9 101 2 S12428 Ig heavy chain V r
45 29 87.9 101 2 S12424 Ig heavy chain V r

ALIGNMENTS

RESULT 1

PH0877

Ig heavy chain V region (anti-DNA, II-1) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 16-Aug-1996

C:Accession: PH0877

R:Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Grossein, C.; Smith, A.; Diamond, B.

J. Exp. Med. 174, 1639-1652, 1991

A:Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype

A:Reference number: PH0862; MUID:92078875; PMID:1660528

A:Accession: PH0877

A:Molecule type: DNA

A:Residues: 1-98 <MAN>

A:Cross-references: UNIPARC:UPI0000176C1P

C:Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:50-66/Region: complementarity-determining 2

Query Match 100.0%; Score 33; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYWIG 5

DB 31 TYWIG 35

RESULT 2

PH1260

Ig heavy chain V region (clone CD-4) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH1260

R:Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.

J. Exp. Med. 176, 1073-1081, 1992

A:Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron

A:Reference number: PH1232; MUID:93018822; PMID:1402653

A:Accession: PH1260

A:Molecule type: DNA

A:Residues: 1-102 <CAI>

A:Cross-references: UNIPARC:UPI0000176B5CF

A:Experimental source: cord blood B cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:19-102/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 33; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Oy 1 TYWIG 5
    |||||
Db 35 TYWIG 39

RESULT 3
PH1263
Ig heavy chain V region (clone VERG2) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1263
R:Ca1, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A:Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chrom
A:Reference number: PH1232; MUID:93018822; PMID:1402653
A:Accession: PH1263
A:Molecule type: mRNA
A:Residues: 1-102 <CAI>
A:Cross-references: UNIPARC:UPI0000176BD0
A:Experimental source: EBV-transformed CD5+ B cell [from adult PBL]
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 33; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 28; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

Oy 1 TYWIG 5
    |||||
Db 35 TYWIG 39

RESULT 4
S19669
Ig heavy chain V region (VH5DJ) - human
C:Species: Homo sapiens (man)
C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C:Accession: S19669
R:Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
J. Mol. Biol. 222, 581-597, 1991
A:Title: BY-passing immunization. Human antibodies from V-gene libraries displayed on ph
A:Reference number: S19663; MUID:92085276; PMID:1748994
A:Accession: S19669
A:Molecule type: mRNA
A:Residues: 1-117 <MAR>
A:Cross-references: UNIPARC:UPI0000115FEA; EMBL:X61651; NID:g37731; PIDN:CAA43832.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 33; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 32; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

Oy 1 TYWIG 5
    |||||
Db 31 TYWIG 35

RESULT 5
S36257
Ig heavy chain V region (clone alpha-CD4-74) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: S36257
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36257
A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA
A:Residues: 1-119 <GRI>
A:Cross-references: UNIPARC:UPI0000118DE9; EMBL:Z18848; NID:g33122; PIDN:CAA79300.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 33; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 33; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

Oy 1 TYWIG 5
    |||||
Db 31 TYWIG 35

RESULT 6
PH1413
Ig heavy chain V region (clone P1-56) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: PH1413
R:van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A:Title: Molecular evolution of the human immunoglobulin E response: High incidence of s
dermatitis.
A:Reference number: PH1409; MUID:93115676; PMID:8418213
A:Accession: PH1413
A:Molecule type: mRNA
A:Residues: 1-123 <VAN>
A:Cross-references: UNIPARC:UPI0000176A34
A:Experimental source: BMC
A>Note: the authors translated the codon CTG for residue 115 as Met
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 33; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 34; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

Oy 1 TYWIG 5
    |||||
Db 31 TYWIG 35

RESULT 7
PH1409
Ig heavy chain V region (clone P1-51) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C:Accession: PH1409
R:van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A:Title: Molecular evolution of the human immunoglobulin E response: High incidence of s
dermatitis.
A:Reference number: PH1409; MUID:93115676; PMID:8418213
A:Accession: PH1409
A:Molecule type: mRNA
A:Residues: 1-127 <VAN>
A:Cross-references: UNIPARC:UPI0000176B99
A:Experimental source: BMC
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 33; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 35; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

Oy 1 TYWIG 5
    |||||
Db 31 TYWIG 35
```

RESULT 8

S57903
probable amino acid permease - Lactobacillus delbrueckii (fragment)
C:Species: Lactobacillus delbrueckii
C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 05-Oct-2004
C:Accession: S57903
R:Vongerichten, K.F.; Klein, J.R.; Matern, H.; Plapp, R.
Microbiology 140, 2591-2600, 1994
A:Title: Cloning and nucleotide sequence analysis of pepV, a carnosinase gene from Lactobacillus delbrueckii
A:Reference number: S57902; MUID:95093606; PMID:7528082
A:Accession: S57903
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-175 <VON>
A:CROSS-references: UNIPROT:P45495; UNIPARC:UPI000013BDC8; EMBL:Z31377; NID:G577568; PID:10000000A669E; UNIPARC:UPI00000A669E; GB:AE002093; NID:G4586069; PI:144-13
C:Genetics:
A:Start codon: TTG
C:Superfamily: ecotropic retrovirus receptor protein

Query Match 100.0%; Score 33; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYWIG 5
|||||
Db 101 TYWIG 105

RESULT 9

F75561
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: F75561
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioreistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: F75561
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-181 <WHI>
A:CROSS-references: UNIPROT:Q9RY56; UNIPARC:UPI00000C16C8; GB:AE001872; GB:AE000513; NID:10000000A669E; UNIPARC:UPI00000A669E; GB:AE002093; NID:G4586069; PI:144-13
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0094
A:Map position: 1

Query Match 100.0%; Score 33; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYWIG 5
|||||
Db 114 TYWIG 118

RESULT 10

E84505
hypothetical protein At2g13130 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004
C:Accession: E84505
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.L.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: E84505
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-324 <STO>
A:CROSS-references: UNIPROT:Q9SL55; UNIPARC:UPI00000A669E; GB:AE002093; NID:G4586069; PI:144-13
C:Genetics:
A:Gene: At2g13130
A:Map position: 2
C:Superfamily: hypothetical protein containing F-box domain

Query Match 100.0%; Score 33; DB 2; Length 324;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYWIG 5
|||||
Db 129 TYWIG 133

RESULT 11

E71105
hypothetical protein PH0614 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C:Accession: E71105
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekir M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaeon Pyrococcus horikoshii
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: E71105
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-332 <KAW>
A:CROSS-references: UNIPROT:O58348; UNIPARC:UPI0000139B2F; GB:AP0000003; NID:G3236130; PI:144-13
A:Experimental source: strain O73
A:Note: This accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH0614

Query Match 100.0%; Score 33; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYWIG 5
|||||
Db 204 TYWIG 208

RESULT 12

G75055
hypothetical protein PAB0953 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 05-Oct-2004
C:Accession: G75055
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str
A:Reference number: A75001
A:Accession: G75055
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-333 <KAW>
A:CROSS-references: UNIPROT:Q9UY52; UNIPARC:UPI0000139E6C; GB:AJ248287; GB:AL096836; NID:10000000A669E; UNIPARC:UPI00000A669E; GB:AE002093; NID:G4586069; PI:144-13
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB0953
C:Superfamily: hypothetical protein PYRAB14350 precursor

Query Match 100.0%; Score 33; DB 2; Length 333;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYWIG 5
 |||||
 Db 204 TYWIG 208

RESULT 13
 E82896
 hemin permease UU399 [imported] - Ureaplasma urealyticum
 C/Species: Ureaplasma urealyticum
 C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C/Accession: E82896
 R/Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
 submitted to GenBank, February 2000
 A/Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
 A/Reference number: A82870
 A/Accession: E82896
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-348 <GLA>
 A/Cross-references: UNIPARC:UPI00000C1C54; GB:AE002137; GB:AF222894; NID:G6899377; PIDN:
 A/Experimental source: serovar 3; biovar 1
 C/Genetics:
 A/Gene: hmuU-2; UU399
 A/Genetic code: SGC3

Query Match 100.0%; Score 33; DB 2; Length 348;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYWIG 5
 |||||
 Db 314 TYWIG 318

RESULT 14
 D82186
 beta-lactamase-related protein VC1562 [imported] - Vibrio cholerae (strain N16961 serogr
 C/Species: Vibrio cholerae
 C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C/Accession: D82186
 R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
 chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, B
 l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A/Reference number: A82035; MUID:20406833; PMID:10952301
 A/Accession: D82186
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-390 <HEI>
 A/Cross-references: UNIPROT:Q9KRS4; UNIPARC:UPI00000C301A; GB:AE004233; GB:AE003852; NID
 A/Experimental source: serogroup O1, strain N16961; biotype El Tor
 C/Genetics:
 A/Gene: VC1562
 A/Map position: 1

Query Match 100.0%; Score 33; DB 2; Length 390;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYWIG 5
 |||||
 Db 100 TYWIG 104

RESULT 15
 A95963
 Probable oxidoreductase protein tauD [imported] - Sinorhizobium melliloti (strain 1021) m
 C/Species: Sinorhizobium melliloti
 C/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 C/Accession: A95963
 R/Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernar
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A/Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endo
 A/Reference number: A95842; MUID:21396508; PMID:111481431
 A/Accession: A95963
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-466 <KUR>
 A/Cross-references: UNIPROT:Q92UW7; UNIPARC:UPI00000CB6FC; GB:AL591985; PIDN:CAC49369.1;
 A/Experimental source: strain 1021, megaplasmid pSymB
 R/Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.;
 A/Title: The composite genome of the legume symbiont Sinorhizobium melliloti.
 A/Reference number: A96039; MUID:21368234; PMID:11474104
 A/Contents: annotation
 C/Genetics:
 A/Gene: tauD; SMB21529
 A/Genome: plasmid

Query Match 100.0%; Score 33; DB 2; Length 466;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYWIG 5
 |||||
 Db 36 TYWIG 40

Search completed: December 3, 2005, 14:33:34
 Job time : 3.36735 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 14:11:48 ; Search time 8.81633 Seconds
(without alignments)
400.126 Million cell updates/sec

Title: US-10-769-144-13
Perfect score: 33
Sequence: 1 TYWIG 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	103	2	Q81Q53 DROME
2	33	100.0	137	2	Q81GH9 DROSOPHILA
3	33	100.0	145	2	Q9VRL1 DROSOPHILA
4	33	100.0	145	2	Q6X125 DROSOPHILA
5	33	100.0	150	2	Q8W1A2 ORYZA
6	33	100.0	166	2	Q9UDK8 HUMAN
7	33	100.0	175	1	YPEV LACDL
8	33	100.0	178	2	Q4MRV1 BACCE
9	33	100.0	178	2	Q6HDH2 BACHK
10	33	100.0	178	2	Q730I4 BACCL1
11	33	100.0	178	2	Q81B88 BACCR
12	33	100.0	178	2	Q81LN5 BACAN
13	33	100.0	178	2	Q634J1 BACCZ
14	33	100.0	181	2	Q9RY56 DEIRA
15	33	100.0	189	2	Q8C634 MOUSE
16	33	100.0	192	2	Q9ND13 ENTHI
17	33	100.0	192	2	Q511T9 ENTHI
18	33	100.0	192	2	Q4QT07 ENTHI
19	33	100.0	192	2	Q58Q64 ENTHI
20	33	100.0	250	2	Q84JP6 ARATH
21	33	100.0	256	2	Q8TDP9 HUMAN
22	33	100.0	268	2	Q8W189 ORYZA
23	33	100.0	281	2	Q75XR6 HORSE
24	33	100.0	303	2	Q67SS6 SYNTH
25	33	100.0	324	2	Q9SL55 ARATH
26	33	100.0	332	1	Y614 PYRHO
27	33	100.0	333	1	Y1435 PYRAB
28	33	100.0	333	2	Q8U3H9 PYRPU
29	33	100.0	341	2	Q554Z3 DICDI
30	33	100.0	348	2	Q9PQ91 UREPA
31	33	100.0	360	2	Q4FQL5_9GAMM

Q8Y009 ralstonia s
Q8D429 vibrio vuln
Q9KR94 vibrio chol
Q7mfk0 vibrio vuln
Q617d4 caenorhabdi
Q88sq8 lactobacill
Q8rh44 paracoccus
Q8rh53 paracoccus
Q6rh61 paracoccus
Q92uw7 rhizobium m
Q7nd75 gloeobacter
P32739 caenorhabdi
Q7nkz5 gloeobacter
Q4li93 gibberella

ALIGNMENTS

RESULT 1

Q81Q53 DROME PRELIMINARY; PRT; 103 AA.
AC Q81Q53;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE CG10640-PB, isoform B.
GN Name=Dv1A; ORFNames=CG10640;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gallo R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brattier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.F., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J.J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";

```
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomic perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Minkler J.S., Millburn G.H., Prochownik S.E.,
RA Smith C.D., Tupy J.L., Whitfield S.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX FlyBase;
DR Ensembl; CG10640; Drosophila melanogaster.
DR FlyBase; FBgn0035601; Uevia.
DR FlyBase; FBgn0035601; Uevia.
DR GO; GO:0004840; F:ubiquitin conjugating enzyme activity; IEA.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR000608; UBO-conjugat_E2.
DR Pfam; PF00179; UQ con; 1.
DR ProDom; PD000461; UBO_conjugat; 1.
DR SMART; SM00212; UBCC; 1.
DR PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
FT NON TER 1
SQ SEQUENCE 103 AA; 12165 MW; 8569382F12E36F7E CRC64;

Query Match 100.0%; Score 33; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. NO. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYWIG 5
DB 4 TYWIG 8

RESULT 2
Q8IGH9 DROME
ID Q8IGH9_DROME PRELIMINARY; PRT; 137 AA.

Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomic perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Minkler J.S., Millburn G.H., Prochownik S.E.,
RA Smith C.D., Tupy J.L., Whitfield S.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX FlyBase;
DR Ensembl; CG10640; Drosophila melanogaster.
DR FlyBase; FBgn0035601; Uevia.
DR FlyBase; FBgn0035601; Uevia.
DR GO; GO:0004840; F:ubiquitin conjugating enzyme activity; IEA.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR000608; UBO-conjugat_E2.
DR Pfam; PF00179; UQ con; 1.
DR ProDom; PD000461; UBO_conjugat; 1.
DR SMART; SM00212; UBCC; 1.
DR PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
FT NON TER 1
SQ SEQUENCE 103 AA; 12165 MW; 8569382F12E36F7E CRC64;

Query Match 100.0%; Score 33; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. NO. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYWIG 5
DB 4 TYWIG 8

RESULT 2
Q8IGH9 DROME
ID Q8IGH9_DROME PRELIMINARY; PRT; 137 AA.
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AC Q8IGH9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RH13862p (Fragment).
GN Name=Uevia; ORFNames=CG10640;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkely;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champagne M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family.
DR EMBL; BT001776; AAN71531.1; -; mRNA.
DR HSSP; P53152; 1JAT.
DR Ensembl; CG10640; Drosophila melanogaster.
DR FlyBase; FBgn0035601; CG10640.
DR FlyBase; FBgn0035601; Uevia.
DR GO; GO:0004840; F:ubiquitin conjugating enzyme activity; IEA.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR000608; UBO-conjugat_E2.
DR Pfam; PF00179; UQ con; 1.
DR ProDom; PD000461; UBO_conjugat; 1.
DR SMART; SM00212; UBCC; 1.
DR PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
FT NON TER 1
SQ SEQUENCE 137 AA; 15891 MW; 9AFC78A7F22EDC3 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. NO. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYWIG 5
DB 38 TYWIG 42

RESULT 3
Q8VRL1 DROME
ID Q8VRL1_DROME PRELIMINARY; PRT; 145 AA.
AC Q8VRL1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE CG10640-PA, isoform A (LD28904p).
GN Name=Uevia; ORFNames=CG10640;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yeung M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.O.,
RA Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
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RA Burtis K.C., Buesam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fodler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glödek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Haddix N.L., Harvey D.A., Heinan T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasbo P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulyov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusseker D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*";
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
RT *melanogaster* euchromatic genome sequence";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomic perspective";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bertencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley *Drosophila* Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "*Drosophila melanogaster* release 4 sequence";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RG FlyBase;

RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuncio J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003566; AAF50784.1; -; Genomic_DNA.
DR EMBL; AY060384; AAL25423.1; -; mRNA.
DR HSRP; P53152; IUA1.
DR Ensemble; CG10640; *Drosophila melanogaster*.
DR FlyBase; FBGN0035601; CG10640.
DR FlyBase; FBGN0035601; Uev1A.
DR GO; GO:0004840; F-ubiquitin conjugating enzyme activity; IEA.
DR GO; GO:0006512; P-ubiquitin cycle; IEA.
DR InterPro; IPR000608; UBQ-conjugat_E2.
DR Pfam; PF00179; UQ_con; 1.
DR PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
SQ SEQUENCE 145 AA; 16669 MW; BDF48A10486E0D8C CRC64;
Query Match 100.0%; Score 33; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TYWIG 5
Db 46 TYWIG 50
RESULT 4
Q6XI25 DROYA PRELIMINARY; PRT; 145 AA.
ID Q6XI25 DROYA PRELIMINARY; PRT; 145 AA.
AC Q6XI25;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Similar to *Drosophila melanogaster* CG10640 (Fragment).
OS *Drosophila yakuba* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; *Drosophila*.
OX NCBI_TaxID=7245;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22887302; PubMed=14525923; DOI=10.1101/gr.1311003;
RA Domazet-Lozo T., Tautz D.;
RT "An evolutionary analysis of orphan genes in *Drosophila*.";
RL Genome Res. 13:2213-2219(2003).
CC -1- SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family.
DR EMBL; AY323007; AARI0030.1; -; mRNA.
DR GO; GO:0004840; F-ubiquitin conjugating enzyme activity; IEA.
DR GO; GO:0006512; P-ubiquitin cycle; IEA.
DR InterPro; IPR000608; UBQ-conjugat_E2.
DR Pfam; PF00179; UQ_con; 1.
DR ProDom; PD000461; UBQ-conjugat; 1.
DR SMART; SM00212; UBCC; 1.
DR PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
FT NON_TER 1
FT NON_TER 145
FT NON_TER 145
SQ SEQUENCE 145 AA; 16669 MW; BDF48A10486E0D8C CRC64;
Query Match 100.0%; Score 33; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TYWIG 5
Db 46 TYWIG 50

```
RESULT 5
Q8WIA2_ORYSA PRELIMINARY; PRT; 150 AA.
ID Q8WIA2_ORYSA PRELIMINARY; PRT; 150 AA.
AC Q8WIA2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative villin-like protein (Fragment).
GN Name=VLN;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Niu X.G., Wang X.C., Liu Q.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF452250; AAL50774.1; -, mRNA.
DR Gramene; Q8WIA2; -.
DR GO; GO:0003779; F-actin binding; IEA.
DR InterPro; IPR007122; Gelsolin.
DR PRINTS; PR00597; GELSOLIN.
FT NON_TER 1 150
FT NON_TER 150 150
SQ SEQUENCE 150 AA; 16496 MW; 92B815FA4D3BF804 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 108 TYWIG 112

RESULT 6
Q9UDK8_HUMAN PRELIMINARY; PRT; 166 AA.
ID Q9UDK8_HUMAN PRELIMINARY; PRT; 166 AA.
AC Q9UDK8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 3 beta-hydroxysteroid dehydrogenase (Fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA McBride M.W., Russell A.J., Vass K., Forster V., Burridge S.M.,
RA Morrison N., Boyd E., Ponder B.A., Sutcliffe R.G.;
RT "New members of the 3 beta-hydroxysteroid dehydrogenase gene family.";
RL Mol. Cell. Probes 9:121-128(1995).
DR Ensembl; ENSG00000187197; Homo sapiens.
DR GO; GO:0030283; F:3(or 17)beta-hydroxysteroid dehydrogenase a. . .; TAS.
DR InterPro; IPR002225; 3beta_HSD.
DR Pfam; PF01073; 3beta_HSD; 2.
FT NON_TER 1 166
FT NON_TER 166 166
FT NON_CONS 53 54
FT NON_TER 166 166
SQ SEQUENCE 166 AA; 19346 MW; 0D2DB98CBA7C812D CRC64;

Query Match 100.0%; Score 33; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 84 TYWIG 88

RESULT 7
YPEV_LACDL STANDARD; PRT; 175 AA.
ID YPEV_LACDL STANDARD; PRT; 175 AA.
AC P45495;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Hypothetical transport protein in pepv 3'region (ORF2) (Fragment).
OS Lactobacillus delbrueckii subsp. lactis.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=29397;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=DSM 7290 / WS87;
RX MEDLINE=95093606; PubMed=7528082;
RA Vongerichten K., Klein J., Matern H., Plapp R.;
RT "Cloning and nucleotide sequence analysis of pepv, a carnosinase gene
from Lactobacillus delbrueckii subsp. lactis DSM 7290, and partial
characterization of the enzyme.";
RL Microbiology 140:2591-2600(1994).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -!- SIMILARITY: Belongs to the amino acid-polyamine-organocation (APC)
superfamily.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC
CC EMBL; Z31377; CAA83253.1; -, Genomic DNA.
CC PIR; S57903; S57903.
CC InterPro; IPR002293; AA/rel_permease1.
CC InterPro; IPR004840; AAC_permease.
CC InterPro; IPR004841; Permease_region.
CC PANTHER; PTHR11785; AA/rel_permease1; 1.
CC Pfam; PF00324; AA_permease; 1.
CC PROSITE; PS00218; AMINO ACID PERMEASE_1; 1.
KW Amino-acid transport; Hypothetical protein; Transmembrane; Transport.
FT TRANSMEM 25 45 Potential.
FT TRANSMEM 46 66 Potential.
FT TRANSMEM 97 117 Potential.
FT TRANSMEM 124 144 Potential.
FT TRANSMEM 155 175 Potential.
FT NON_TER 175 175
SQ SEQUENCE 175 AA; 19239 MW; A3BABF17736B9C63 CRC64;

Query Match 100.0%; Score 33; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 101 TYWIG 105

RESULT 8
Q4MRV1_BACCE PRELIMINARY; PRT; 178 AA.
ID Q4MRV1_BACCE PRELIMINARY; PRT; 178 AA.
AC Q4MRV1;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORENAMES-BCE_G9241_4402;
OS Bacillus cereus G9241.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=269801;
RN [1]
RP NUCLEOTIDE SEQUENCE.
```

```
RC STRAIN=G9241;
RX PubMed=15155910; DOI=10.1073/pnas.0402414101;
RA Hoffmaster A.R., Ravel J., Raske D.A., Chapman G.D., Chute M.D.,
RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
RA Malden M.C.J., Prieston E.G., Barker M., Jiang L., Cer R.Z.,
RA Rillstone J., Peterson S.N., Meyant R.S., Galloway D.R., Read T.D.,
RA Popovic T., Fraser C.M.;
RT "Identification of anthrax toxin genes in a Bacillus cereus associated
RT with an illness resembling inhalation anthrax.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBSJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAEX01000010; EAL14898.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 178 AA; 20245 MW; 7335039A2DE9847A CRC64;

Query Match 100.0%; Score 33; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 32 TYWIG 36

RESULT 9
Q6HDH2_BACHK
ID Q6HDH2_BACHK PRELIMINARY; PRT; 178 AA.
AC Q6HDH2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=B79727.4086;
OS Bacillus thuringiensis (subsp. konkukian).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=180856;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=97-27;
RA Brittin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RA "Complete genome sequence of Bacillus thuringiensis 97-27.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AE017355; AAT62860.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 178 AA; 20384 MW; 0EA5F67C129A1802 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 32 TYWIG 36

RESULT 10
Q73014_BACCI
ID Q73014_BACCI PRELIMINARY; PRT; 178 AA.
AC Q73014;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BC2432;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=222523;
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[1]
RN NUCLEOTIDE SEQUENCE.
RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Raske D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXOI.1";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AE017278; AAS43333.1; -; Genomic_DNA.
KW TIGR; BC8432; -.
KW Complete proteome.
SQ SEQUENCE 178 AA; 20187 MW; A4F6FCB8B6E51192 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 32 TYWIG 36

RESULT 11
Q81B88_BACCR
ID Q81B88_BACCR PRELIMINARY; PRT; 178 AA.
AC Q81B88;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BC4347;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=226900;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapatral V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Walunas T.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
DR EMBL; AE017012; AAP11260.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 178 AA; 20184 MW; 66CAC78EF69F1489 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 32 TYWIG 36

RESULT 12
Q81LN5_BACAN
ID Q81LN5_BACAN PRELIMINARY; PRT; 178 AA.
AC Q81LN5; Q6HT42; Q6KMD0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BA4579, BAS4248, GBAA4579;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1392;
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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.B., Tetelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holzapple E.K., Okstad O.A., Helgason B., Rilstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423:81-86(2003).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ames / isolate 0581;
RA Rayel J., Raeko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics."
RL Submitted (MAY-2004) to the ENBL/GenBank/DBJ databases.
[3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Stearns;
RA Brettn T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Rice H.,
RT "Complete genome sequence of Bacillus anthracis Sterne."
RL Submitted (JAN-2004) to the ENBL/GenBank/DBJ databases.
DR EMBL; AE017038; AAP28286.1; -; Genomic DNA.
DR EMBL; AE017334; AAT33699.1; -; Genomic DNA.
DR EMBL; AE017225; AAT56547.1; -; Genomic DNA.
DR TIGR; BA579; -.
DR TIGR; GBAA4579; -.
RW Complete proteome; Hypothetical protein.
SQ SEQUENCE 178 AA; 20212 MW; 73CF86EC8583764C CRC64;

Query Match 100.0%; Score 33; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 32 TYWIG 36
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RESULT 13
Q634J1_BACCCZ PRELIMINARY; PRT; 178 AA.
AC Q634J1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Hypothetical protein.
GN ORFNames=BCE33L4097;
OS Bacillus cereus (strain ZK).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=288681;
[1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Brettn T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Rice H.;
RT "Complete genome sequence of Bacillus cereus ZK."
RL Submitted (JUL-2004) to the ENBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU16170.1; -; Genomic DNA.
RW Complete proteome; Hypothetical protein.
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SQ SEQUENCE 178 AA; 20371 MW; E31E967C0C6BFF2A CRC64;

Query Match 100.0%; Score 33; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 32 TYWIG 36
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RESULT 14
Q9RY56_DEIRA PRELIMINARY; PRT; 181 AA.
AC Q9RY56;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein DR0094.
GN OrderedLocustNames=DR0094;
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
[1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RI / ATCC 13939 / DSM 20539 / NCIB 9279;
RX MEDLINE=20036896; PubMed=10567286; DOI=10.1126/science.286.5444.1571;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L.A., Utterback T.R., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans RI."
RL Science 286:1571-1577(1999).
DR EMBL; AE001872; AAF09690.1; -; Genomic DNA.
DR TIGR; DR0094; -.
RW Complete proteome; Hypothetical protein.
SQ SEQUENCE 181 AA; 19371 MW; E29394CD96C746A4 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 114 TYWIG 118
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RESULT 15
Q8C634_MOUSE PRELIMINARY; PRT; 189 AA.
AC Q8C634;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:4922502D21 product:hypothetical C-type lectin domain
DE containing protein, full insert sequence (similar to C lectin-related
DE protein A).
GN Name=4922502D21Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
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RX MEDLINE=92279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glessi C., King B., Kouchiwa H.,
RA Kuehl P., Lewis S., Matsumoto Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yananaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Knapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kurogaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Nunata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempole C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagakawa S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer.";
RN Genome Res. 10:1757-1771(2000).
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Iehil Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Oheato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka I.,
RA Tonaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX Director MGC Project;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK076635; BAC36425.1; -; mRNA.
DR EMBL; BC089479; AA89479.1; -; mRNA.
DR Ensembl; ENSMUSG0000047720; Mus musculus.
DR MGI; MGI:2685920; 4922502D2Rik.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; LECTIN_C.
DR Pfam; PF00059; LECTIN_C; 1.
DR SMART; SM00034; LECTIN_1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
RW Hypothetical protein; LECTIN.
SQ SEQUENCE 189 AA; 22107 MW; 2E5673DBAC2B39E CRC64;
Query Match 100.0%; Score 33; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TYWIG 5
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Db 127 TWIG 131

Search completed: December 3, 2005, 14:32:23
Job time : 11.8163 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 13:24:58 ; Search time 2.12245 Seconds
(without alignments)
194.765 Million cell updates/sec

Title: US-10-769-144-13

Perfect score: 33

Sequence: 1 TYWIG 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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3: /cgn2_6/ptodata/1/iaa/H_COMB pep.*
4: /cgn2_6/ptodata/1/iaa/PCTRUS_COMB pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	33	100.0	88	2	US-09-196-522-172
3	33	100.0	151	2	US-09-270-767-44527
4	33	100.0	430	2	US-09-328-352-5453
5	32	97.0	483	2	US-09-902-540-11130
6	32	97.0	415	2	US-09-902-540-9936
7	32	97.0	616	2	US-09-540-236-3084
8	31	93.9	5	2	US-09-920-262A-1
9	31	93.9	110	2	US-09-252-991A-18248
10	31	93.9	119	2	US-09-920-262A-7
11	31	93.9	315	2	US-09-603-208A-212
12	31	93.9	483	2	US-09-603-208A-210
13	31	93.9	484	2	US-09-328-352-4849
14	31	93.9	488	2	US-09-328-352-4928
15	30	90.9	476	2	US-09-328-352-5950
16	29	87.9	8	2	US-08-444-818-602
17	29	87.9	8	2	US-08-444-818-603
18	29	87.9	8	2	US-08-444-818-604
19	29	87.9	98	1	US-08-478-039-81
20	29	87.9	98	1	US-08-476-349A-81
21	29	87.9	98	1	US-08-665-202-33
22	29	87.9	98	2	US-09-315-574-33
23	29	87.9	98	2	US-10-194-975-45
24	29	87.9	117	2	US-08-545-809A-133
25	29	87.9	117	2	US-09-515-697-133
26	29	87.9	119	2	US-09-025-769B-26
27	29	87.9	119	2	US-09-490-070A-26

28	29	87.9	119	2	US-09-490-153-26	Sequence 26, Appl
29	29	87.9	119	2	US-09-490-324-26	Sequence 26, Appl
30	29	87.9	120	2	US-09-025-769B-40	Sequence 40, Appl
31	29	87.9	120	2	US-09-025-769B-67	Sequence 67, Appl
32	29	87.9	120	2	US-09-490-070A-40	Sequence 40, Appl
33	29	87.9	120	2	US-09-490-070A-67	Sequence 67, Appl
34	29	87.9	120	2	US-09-490-153-40	Sequence 40, Appl
35	29	87.9	120	2	US-09-490-153-67	Sequence 67, Appl
36	29	87.9	120	2	US-09-490-324-40	Sequence 40, Appl
37	29	87.9	120	2	US-09-490-324-67	Sequence 67, Appl
38	29	87.9	121	1	US-08-388-672A-20	Sequence 20, Appl
39	29	87.9	121	1	US-08-388-672A-23	Sequence 23, Appl
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41	29	87.9	122	2	US-08-983-607-30	Sequence 30, Appl
42	29	87.9	126	2	US-09-080-554-20	Sequence 20, Appl
43	29	87.9	131	2	US-09-291-922-6	Sequence 6, Appl
44	29	87.9	165	2	US-09-902-540-9847	Sequence 9847, Ap
45	29	87.9	193	2	US-09-543-681A-4479	Sequence 4479, Ap

ALIGNMENTS

RESULT 1

US-09-726-219A-172
; Sequence 172, Application US/09726219A
; Patent No. 6806079
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clarkson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 213839-00013
; CURRENT APPLICATION NUMBER: US/09/726,219A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 172
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-726-219A-172

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Query Match      100.0%; Score 33; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 31 TYWIG 35

RESULT 2
US-09-196-522-172
; Sequence 172, Application US/09196522
; Patent No. 6916605
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clarkson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 213839-00004
; CURRENT APPLICATION NUMBER: US/09/196,522
; CURRENT FILING DATE: 1998-11-28
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 172
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-196-522-172

Query Match      100.0%; Score 33; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 31 TYWIG 35

RESULT 3
US-09-270-767-44527
; Sequence 44527, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
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; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44527
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-44527

Query Match      100.0%; Score 33; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 52 TYWIG 56

RESULT 4
US-09-328-352-5453
; Sequence 5453, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GPC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5453
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5453

Query Match      100.0%; Score 33; DB 2; Length 430;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 185 TYWIG 189

RESULT 5
US-09-902-540-11130
; Sequence 11130, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11130
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11130

Query Match      97.0%; Score 32; DB 2; Length 383;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
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Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5

Db 295 TYWVG 299

RESULT 6

US-09-902-540-9936
; Sequence 9936, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 9936
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-9936

Query Match 97.0%; Score 32; DB 2; Length 415;

Best Local Similarity 80.0%; Pred. No. 3.7e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5

Db 58 TYWVG 62

RESULT 7

US-09-540-236-3084
; Sequence 3084, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Berton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 3084
; LENGTH: 616
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-3084

Query Match 97.0%; Score 32; DB 2; Length 616;

Best Local Similarity 80.0%; Pred. No. 5.4e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5

Db 593 TYWVG 597

RESULT 8

US-09-920-262A-1
; Sequence 1, Application US/09920262A
; Patent No. 6902734
; GENERAL INFORMATION:
; APPLICANT: Shealy, David
; APPLICANT: Knight, David
; APPLICANT: Scallion, Bernie

; APPLICANT: Giles-Komar, Jill
; APPLICANT: Peritt, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0248
; CURRENT APPLICATION NUMBER: US/09/920,262A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,827
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-262A-1

Query Match 93.9%; Score 31; DB 2; Length 5;

Best Local Similarity 80.0%; Pred. No. 4.6e+05;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5

Db 1 TYWLG 5

RESULT 9

US-09-252-991A-18248
; Sequence 18248, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18248
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18248

Query Match 93.9%; Score 31; DB 2; Length 110;

Best Local Similarity 80.0%; Pred. No. 1.6e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5

Db 85 TYWLG 89

RESULT 10

US-09-920-262A-7
; Sequence 7, Application US/09920262A
; Patent No. 6902734
; GENERAL INFORMATION:
; APPLICANT: Shealy, David
; APPLICANT: Knight, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Peritt, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0248
; CURRENT APPLICATION NUMBER: US/09/920,262A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/223,358

1 PRIOR FILING DATE: 2000-08-07
1 PRIOR APPLICATION NUMBER: 60/236,827
1 PRIOR FILING DATE: 2000-09-29
1 NUMBER OF SEQ ID NOS: 15
1 SOFTWARE: PatentIn Ver 3.1
1 SEQ ID NO 7
1 LENGTH: 119
1 TYPE: PRT
1 ORGANISM: Homo sapiens
US-09-920-262A-7

Query Match 93.9%; Score 31; DB 2; Length 119;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
|||:
Db 31 TYWIG 35

RESULT 11
US-09-603-208A-212
1 Sequence 212, Application US/09603208A
1 Patent No. 6822084
1 GENERAL INFORMATION:
1 APPLICANT: Pompejus, Markus
1 APPLICANT: Kroger, Burkhard
1 APPLICANT: Schroder, Hartwig
1 APPLICANT: Zelder, Oskar
1 APPLICANT: Haberhauer, Gregor
1 APPLICANT: Lee, Heung-Shick
1 APPLICANT: Kim, Hyung-Joon
1 TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,
1 TITLE OF INVENTION: RESISTANCE AND TOLERANCE PROTEINS
1 FILE REFERENCE: BGI-124CP
1 CURRENT APPLICATION NUMBER: US/09/603,208A
1 CURRENT FILING DATE: 2000-06-23
1 PRIOR APPLICATION NUMBER: 60/141031
1 PRIOR FILING DATE: 1999-06-25
1 PRIOR APPLICATION NUMBER: 60/142692
1 PRIOR FILING DATE: 1999-07-01
1 PRIOR APPLICATION NUMBER: 60/151214
1 PRIOR FILING DATE: 1999-08-27
1 PRIOR APPLICATION NUMBER: DE 19930429.7
1 PRIOR FILING DATE: 1999-07-01
1 PRIOR APPLICATION NUMBER: DE 19931413.6
1 PRIOR FILING DATE: 1999-07-08
1 PRIOR APPLICATION NUMBER: DE 19931457.8
1 PRIOR FILING DATE: 1999-07-08
1 PRIOR APPLICATION NUMBER: DE 19931541.8
1 PRIOR FILING DATE: 1999-07-08
1 PRIOR APPLICATION NUMBER: DE 19932209.0
1 PRIOR FILING DATE: 1999-07-09
1 PRIOR APPLICATION NUMBER: DE 19932230.9
1 PRIOR FILING DATE: 1999-07-14
1 PRIOR APPLICATION NUMBER: DE 19940764.9
1 PRIOR FILING DATE: 1999-08-27
1 PRIOR APPLICATION NUMBER: DE 19941382.7
1 PRIOR FILING DATE: 1999-08-31
1 NUMBER OF SEQ ID NOS: 306
1 SEQ ID NO 212
1 LENGTH: 315
1 TYPE: PRT
1 ORGANISM: Corynebacterium glutamicum
US-09-603-208A-212

Query Match 93.9%; Score 31; DB 2; Length 315;
Best Local Similarity 80.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5

Db 129 TYWIG 133
|||:
|||:

RESULT 12
US-09-603-208A-210
1 Sequence 210, Application US/09603208A
1 Patent No. 6822084
1 GENERAL INFORMATION:
1 APPLICANT: Pompejus, Markus
1 APPLICANT: Kroger, Burkhard
1 APPLICANT: Schroder, Hartwig
1 APPLICANT: Zelder, Oskar
1 APPLICANT: Haberhauer, Gregor
1 APPLICANT: Lee, Heung-Shick
1 APPLICANT: Kim, Hyung-Joon
1 TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,
1 TITLE OF INVENTION: RESISTANCE AND TOLERANCE PROTEINS
1 FILE REFERENCE: BGI-124CP
1 CURRENT APPLICATION NUMBER: US/09/603,208A
1 CURRENT FILING DATE: 2000-06-23
1 PRIOR APPLICATION NUMBER: 60/141031
1 PRIOR FILING DATE: 1999-06-25
1 PRIOR APPLICATION NUMBER: 60/142692
1 PRIOR FILING DATE: 1999-07-01
1 PRIOR APPLICATION NUMBER: 60/151214
1 PRIOR FILING DATE: 1999-08-27
1 PRIOR APPLICATION NUMBER: DE 19930429.7
1 PRIOR FILING DATE: 1999-07-01
1 PRIOR APPLICATION NUMBER: DE 19931413.6
1 PRIOR FILING DATE: 1999-07-08
1 PRIOR APPLICATION NUMBER: DE 19931457.8
1 PRIOR FILING DATE: 1999-07-08
1 PRIOR APPLICATION NUMBER: DE 19931541.8
1 PRIOR FILING DATE: 1999-07-08
1 PRIOR APPLICATION NUMBER: DE 19932209.0
1 PRIOR FILING DATE: 1999-07-09
1 PRIOR APPLICATION NUMBER: DE 19932230.9
1 PRIOR FILING DATE: 1999-07-14
1 PRIOR APPLICATION NUMBER: DE 19940764.9
1 PRIOR FILING DATE: 1999-08-27
1 PRIOR APPLICATION NUMBER: DE 19941382.7
1 PRIOR FILING DATE: 1999-08-31
1 NUMBER OF SEQ ID NOS: 306
1 SEQ ID NO 210
1 LENGTH: 483
1 TYPE: PRT
1 ORGANISM: Corynebacterium glutamicum
US-09-603-208A-210

Query Match 93.9%; Score 31; DB 2; Length 483;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
|||:
|||:

Db 129 TYWIG 133

RESULT 13
US-09-328-352-4849
1 Sequence 4849, Application US/09328352
1 Patent No. 6562958
1 GENERAL INFORMATION:
1 APPLICANT: Gary L. Breton et al.
1 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
1 TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
1 FILE REFERENCE: GTC99-03PA
1 CURRENT APPLICATION NUMBER: US/09/328,352
1 CURRENT FILING DATE: 1999-06-04
1 NUMBER OF SEQ ID NOS: 8252

Query Match 93.9%; Score 31; DB 2; Length 315;
Best Local Similarity 80.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5

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; SEQ ID NO 4849
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4849

Query Match      93.9%; Score 31; DB 2; Length 484;
Best Local Similarity 80.0%; Pred. NO. 6.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TYWIG 5
      |||||
Db      111 TYWLG 115

RESULT 14
US-09-328-352-4928
; Sequence 4928, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4928
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4928

Query Match      93.9%; Score 31; DB 2; Length 488;
Best Local Similarity 80.0%; Pred. NO. 6.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TYWIG 5
      |||||
Db      112 TYWLG 116

RESULT 15
US-09-328-352-5950
; Sequence 5950, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5950
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5950

Query Match      90.9%; Score 30; DB 2; Length 476;
Best Local Similarity 80.0%; Pred. NO. 9.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TYWIG 5
      |||||
Db      257 TYWVG 261

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Job time : 2.12245 secs
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OM protein - protein search, using sw model

Run on: December 3, 2005, 13:27:13 ; Search time 6.85714 Seconds
(without alignments)
304.667 Million cell updates/sec

Title: US-10-769-144-13

Perfect score: 33

Sequence: 1 TYWIG 5

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Total number of hits satisfying chosen parameters: 1867569

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	5	4	US-10-374-932-5
2	33	100.0	5	4	US-10-379-741-5
3	33	100.0	5	5	US-10-769-144-13
4	33	100.0	5	5	US-10-891-658-92
5	33	100.0	5	5	US-10-982-725-5
6	33	100.0	5	5	US-10-903-191-13
7	33	100.0	76	4	US-10-437-963-106931
8	33	100.0	88	4	US-10-803-622-172
9	33	100.0	88	4	US-10-803-653-172
10	33	100.0	116	3	US-09-851-614-4
11	33	100.0	116	4	US-10-035-637-4
12	33	100.0	116	5	US-10-769-144-4
13	33	100.0	116	5	US-10-903-191-4
14	33	100.0	125	5	US-10-891-658-79
15	33	100.0	130	4	US-10-226-615-2
16	33	100.0	130	4	US-10-374-932-2
17	33	100.0	130	4	US-10-379-741-2
18	33	100.0	130	5	US-10-982-725-2
19	33	100.0	145	6	US-11-097-143-22335
20	33	100.0	248	3	US-09-880-748-1
21	33	100.0	248	4	US-10-293-418-1
22	33	100.0	373	4	US-10-114-270-92
23	33	100.0	393	4	US-10-425-115-208389
24	33	100.0	411	5	US-10-769-144-12
25	33	100.0	411	5	US-10-903-191-12
26	33	100.0	468	5	US-10-769-144-2
27	33	100.0	468	5	US-10-903-191-2

Sequence 8, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 126524,
Sequence 3838, Ap
Sequence 262693,
Sequence 880, App
Sequence 48326, A
Sequence 165309,
Sequence 22427, A
Sequence 142529,
Sequence 48506, A
Sequence 4, Appli
Sequence 2, Appli
Sequence 8, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-10-374-932-5

; Sequence 5, Application US/10374932

; Publication No. US20030235586A1

; GENERAL INFORMATION:

; APPLICANT: van de Winkel, Jan G.J.

; APPLICANT: van Dijk, Marcus Antonius

; APPLICANT: Schuurman, Janine

; APPLICANT: Gerritsen, Arnout F.

; APPLICANT: Baadsgaard, Ole

; APPLICANT: Petersen, Jorgen

; TITLE OF INVENTION: HUMAN ANTIBODIES SPECIFIC FOR INTERLEUKIN 15 (IL-15)

; FILE REFERENCE: GMI-024CP

; CURRENT APPLICATION NUMBER: US/10/374,932

; CURRENT FILING DATE: 2003-02-26

; PRIOR APPLICATION NUMBER: US 60/314,731

; PRIOR FILING DATE: 2001-08-23

; PRIOR APPLICATION NUMBER: US 10/226615

; PRIOR FILING DATE: 2002-08-23

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-374-932-5

Query Match 100.0%; Score 33; DB 4; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYWIG 5

Db 1 TYWIG 5

RESULT 2

US-10-379-741-5

; Sequence 5, Application US/10379741

; Publication No. US20040071702A1

; GENERAL INFORMATION:

; APPLICANT: van de Winkel, Jan G.J.

; APPLICANT: van Dijk, Marcus Antonius

; APPLICANT: Schuurman, Janine

; APPLICANT: Gerritsen, Arnout F.

; APPLICANT: Baadsgaard, Ole

; APPLICANT: Petersen, Jorgen

; TITLE OF INVENTION: HUMAN ANTIBODIES SPECIFIC FOR INTERLEUKIN 15 (IL-15)

; FILE REFERENCE: GMI-024CP2

; CURRENT APPLICATION NUMBER: US/10/379,741

; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: US 60/314,731
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: US 10/226615
; PRIOR FILING DATE: 2002-08-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-379-741-5

Query Match 100.0%; Score 33; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 1 TYWIG 5

RESULT 3

US-10-769-144-13
; Sequence 13, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-13

Query Match 100.0%; Score 33; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 1 TYWIG 5

RESULT 4

US-10-891-658-92
; Sequence 92, Application US/10891658
; Publication No. US20050074821A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth, Wild
; APPLICANT: Treanor, James
; APPLICANT: Huang, Haichun
; APPLICANT: Inoue, Heather
; APPLICANT: Zhang, Tie J.
; APPLICANT: Martin, Frank
; TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway
; FILE REFERENCE: 02-1240
; CURRENT APPLICATION NUMBER: US/10/891,658
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/487,431
; PRIOR FILING DATE: 2003-07-15

; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 92
; LENGTH: 5
; TYPE: PRT
; ORGANISM: homo sapien
US-10-891-658-92

Query Match 100.0%; Score 33; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 1 TYWIG 5

RESULT 5

US-10-982-725-5
; Sequence 5, Application US/10982725
; Publication No. US20050123542A1
; GENERAL INFORMATION:
; APPLICANT: BEURSKENS, Frank
; APPLICANT: SCHURMAN, Janine
; APPLICANT: PARREN, Paul
; APPLICANT: PETERSEN, Jorgen
; APPLICANT: BAADSGAARD, Ole
; TITLE OF INVENTION: METHODS FOR TREATING DISORDERS INVOLVING MONOCYTES
; FILE REFERENCE: AMJ-002
; CURRENT APPLICATION NUMBER: US/10/982,725
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/518552
; PRIOR FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-982-725-5

Query Match 100.0%; Score 33; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 1 TYWIG 5

RESULT 6

US-10-903-191-13
; Sequence 13, Application US/10903191
; Publication No. US20050180983A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301CP
; CURRENT APPLICATION NUMBER: US/10/903,191
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/769144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 5
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-903-191-13

Query Match      100.0%; Score 33; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYWIG 5
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Db 1 TYWIG 5

RESULT 7
US-10-437-963-106931
; Sequence 106931, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 106931
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_11330C.1.pgp
US-10-437-963-106931

Query Match      100.0%; Score 33; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYWIG 5
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Db 9 TYWIG 13

RESULT 8
US-10-803-622-172
; Sequence 172, Application US/10803622
; Publication No. US20040157214A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,622
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
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; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 172
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-803-622-172

Query Match      100.0%; Score 33; DB 4; Length 88;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYWIG 5
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Db 31 TYWIG 35

RESULT 9
US-10-803-653-172
; Sequence 172, Application US/10803653
; Publication No. US20040157215A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,653
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
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; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 172
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-803-653-172

Query Match      100.0%; Score 33; DB 4; Length 88;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TYWIG 5
Db      31 TYWIG 35

RESULT 10
US-09-851-614-4
; Sequence 4, Application US/09851614
; Publication No. US20030167502A1
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Keler, Tibor
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: MXI-166
; CURRENT APPLICATION NUMBER: US/09/851,614
; PRIOR FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: USN 60/203,126
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: USN 60/230,739
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-851-614-4

Query Match      100.0%; Score 33; DB 3; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TYWIG 5
Db      31 TYWIG 35

RESULT 11
US-10-035-637-4
; Sequence 4, Application US/10035637
; Publication No. US20030031667A1
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Keler, Tibor
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: MXI-166CP
; CURRENT APPLICATION NUMBER: US/10/035,637
; CURRENT FILING DATE: 2001-11-07
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 09/851,614
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USN 60/203,126
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: USN 60/230,739
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-903-191-4

; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-035-637-4

Query Match      100.0%; Score 33; DB 4; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TYWIG 5
Db      31 TYWIG 35

RESULT 12
US-10-769-144-4
; Sequence 4, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-4

Query Match      100.0%; Score 33; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TYWIG 5
Db      31 TYWIG 35

RESULT 13
US-10-903-191-4
; Sequence 4, Application US/10903191
; Publication No. US20050180983A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301CP
; CURRENT APPLICATION NUMBER: US/10/903,191
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/769144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-903-191-4
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Query Match 100.0%; Score 33; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
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|
|
|
Db 31 TYWIG 35

RESULT 14
US-10-891-658-79
; Sequence 79, Application US/10891658
; Publication No. US20050074821A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth, Wild
; APPLICANT: Treanor, James
; APPLICANT: Huang, Haichun
; APPLICANT: Inoue, Heather
; APPLICANT: Zhang, Tie J.
; APPLICANT: Martin, Frank
; TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: 02-1240
; CURRENT APPLICATION NUMBER: US/10/891,658
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/487,431
; PRIOR FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 79
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapien
US-10-891-658-79

Query Match 100.0%; Score 33; DB 5; Length 125;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
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|
|
|
Db 31 TYWIG 35

RESULT 15
US-10-226-615-2
; Sequence 2, Application US/10226615
; Publication No. US20030138421A1
; GENERAL INFORMATION:
; APPLICANT: van de Winkel, Jan G.J.
; APPLICANT: van Dijk, Marcus Antonius
; APPLICANT: Gerritsen, Arnout F.
; APPLICANT: Schuurman, Janine
; APPLICANT: Baadsgaard, Ole
; TITLE OF INVENTION: HUMAN ANTIBODIES SPECIFIC FOR INTERLEUKIN 15 (IL-15)
; FILE REFERENCE: GMI-024
; CURRENT APPLICATION NUMBER: US/10/226,615
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: US 60/314,731
; PRIOR FILING DATE: 2001-08-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-226-615-2

Query Match 100.0%; Score 33; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
|
|
|
|
Db 31 TYWIG 35

Search completed: December 3, 2005, 14:17:34
Job time : 6.85714 secs

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OM protein - protein search, using sw model

Run on: December 3, 2005, 13:48:29 ; Search time 0.285714 Seconds
(without alignments)
83.796 Million cell updates/sec

Title: US-10-769-144-13

Perfect score: 33

Sequence: 1 TYWIG 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Published Applications AA New:*

- 1: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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- 5: /cgn2_6/ptodata/1/pubpaa/FCT_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	29	87.9	98	7 US-11-054-669-45	Sequence 45, Appl
3	29	87.9	98	7 US-11-084-554-56	Sequence 56, Appl
4	29	87.9	252	7 US-11-054-515-1537	Sequence 1537, Ap
5	28	84.8	157	6 US-10-793-626-1168	Sequence 1168, Ap
6	28	84.8	163	6 US-10-467-657-6140	Sequence 6140, Ap
7	28	84.8	249	7 US-11-054-515-1312	Sequence 1312, Ap
8	28	84.8	254	7 US-11-054-515-873	Sequence 873, Ap
9	28	84.8	254	7 US-11-054-515-888	Sequence 888, Ap
10	28	84.8	254	7 US-11-054-515-1087	Sequence 1087, Ap
11	28	84.8	254	7 US-11-054-515-1088	Sequence 1088, Ap
12	28	84.8	372	6 US-10-844-035-1	Sequence 1, Appli
13	28	84.8	582	7 US-11-074-176-110	Sequence 110, App
14	27	81.8	117	6 US-10-821-234-1253	Sequence 1253, Ap
15	27	81.8	314	7 US-11-108-172-1110	Sequence 1110, Ap
16	27	81.8	372	6 US-10-131-826A-106	Sequence 106, App
17	27	81.8	416	6 US-10-821-234-1375	Sequence 1375, Ap
18	26	78.8	118	6 US-10-793-626-2630	Sequence 2630, Ap
19	26	78.8	130	6 US-10-467-657-3470	Sequence 3470, Ap
20	26	78.8	163	6 US-10-467-657-8522	Sequence 8522, Ap
21	26	78.8	178	6 US-10-467-657-2108	Sequence 2108, Ap
22	26	78.8	232	6 US-10-793-626-1602	Sequence 1602, Ap
23	26	78.8	244	6 US-10-821-234-1264	Sequence 1264, Ap
24	26	78.8	253	7 US-11-054-515-1003	Sequence 1003, Ap
25	26	78.8	253	7 US-11-054-515-1007	Sequence 1007, Ap

26	26	78.8	265	6 US-10-689-742-188	Sequence 188, App
27	26	78.8	293	6 US-10-131-826A-422	Sequence 422, App
28	26	78.8	361	6 US-10-821-234-1166	Sequence 1166, Ap
29	26	78.8	433	6 US-10-131-826A-6	Sequence 6, Appli
30	26	78.8	491	6 US-10-131-826A-278	Sequence 278, App
31	26	78.8	493	6 US-10-131-826A-268	Sequence 268, App
32	26	78.8	493	7 US-11-067-121-10	Sequence 10, Appl
33	26	78.8	493	7 US-11-067-121-20	Sequence 20, Appl
34	26	78.8	496	7 US-11-067-121-3	Sequence 3, Appli
35	26	78.8	496	7 US-11-067-121-12	Sequence 12, Appl
36	26	78.8	501	7 US-11-055-822-52	Sequence 52, Appl
37	26	78.8	515	6 US-10-467-657-1968	Sequence 1968, Ap
38	26	78.8	613	6 US-10-131-826A-190	Sequence 190, App
39	26	78.8	617	6 US-10-982-545-2	Sequence 2, Appli
40	26	78.8	782	6 US-10-821-234-1592	Sequence 1592, Ap
41	26	78.8	2323	6 US-10-793-626-760	Sequence 760, App
42	25	75.8	146	6 US-10-793-626-2694	Sequence 2694, Ap
43	25	75.8	148	6 US-10-512-109-21	Sequence 21, Appl
44	25	75.8	214	6 US-10-793-626-1898	Sequence 1898, Ap
45	25	75.8	224	6 US-10-793-626-1002	Sequence 1002, Ap

ALIGNMENTS

RESULT 1

US-11-054-515-1
; Sequence 1, Application US/11054515
; Publication No US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1

Query Match 100.0%; Score 33; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 6.1; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 TYWIG 5
Db 31 TYWIG 35

RESULT 2

US-11-054-669-45
; Sequence 45, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-45

Query Match 87.9%; Score 29; DB 7; Length 98;
Best Local Similarity 80.0%; Pred. No. 15;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
:||||
Db 31 SYWIG 35

RESULT 3
US-11-084-554-56
; Sequence 56, Application US/11084554
; Publication No. US2005026079A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-56

Query Match 87.9%; Score 29; DB 7; Length 98;
Best Local Similarity 80.0%; Pred. No. 15;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
:||||
Db 31 SYWIG 35

RESULT 4
US-11-054-515-1537
; Sequence 1537, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515

; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 03/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1537
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1537

Query Match 87.9%; Score 29; DB 7; Length 252;
Best Local Similarity 80.0%; Pred. No. 32;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
:||||
Db 31 SYWIG 35

RESULT 5
US-10-793-626-1168
; Sequence 1168, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1168
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1168

Query Match 84.8%; Score 28; DB 6; Length 157;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YWIG 5
:||||
Db 112 YWIG 115

RESULT 6
US-10-467-657-6140
; Sequence 6140, Application US/10467657

Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNAGNI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6140
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6140

Query Match 84.8%; Score 28; DB 6; Length 163;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YWIG 5
Db 113 YWIG 116

RESULT 7

US-11-054-515-1312
; Sequence 1312, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1312
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1312

Query Match 84.8%; Score 28; DB 7; Length 249;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YWIG 5

Db 32 YWIG 35

RESULT 8

US-11-054-515-873
; Sequence 873, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 873
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-873

Query Match 84.8%; Score 28; DB 7; Length 254;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YWIG 5
Db 32 YWIG 35

RESULT 9

US-11-054-515-888
; Sequence 888, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15

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; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 888
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-888

Query Match      84.8%; Score 28; DB 7; Length 254;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 YWIG 5
Db      32 YWIG 35

RESULT 10
US-11-054-515-1087
; Sequence 1087, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1087
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1087

Query Match      84.8%; Score 28; DB 7; Length 254;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 YWIG 5
Db      32 YWIG 35

RESULT 11
US-11-054-515-1087

Query Match      84.8%; Score 28; DB 7; Length 254;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 YWIG 5
Db      32 YWIG 35
```

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US-11-054-515-1088
; Sequence 1088, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1088
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1088

Query Match      84.8%; Score 28; DB 7; Length 254;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 YWIG 5
Db      32 YWIG 35

RESULT 12
US-10-844-035-1
; Sequence 1, Application US/10844035
; Publication No. US20050255098A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN, STEVEN D.
; APPLICANT: NOBLE, LINDA J.
; TITLE OF INVENTION: METHODS OF TREATING TRAUMATIC SPINAL
; TITLE OF INVENTION: CORD INJURY
; FILE REFERENCE: UCAL-319
; CURRENT APPLICATION NUMBER: US/10/844,035
; CURRENT FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 372
; TYPE: PRT
; ORGANISM: homo sapien
US-10-844-035-1

Query Match      84.8%; Score 28; DB 6; Length 372;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 YWIG 5
Db      87 YWIG 90
```

RESULT 13

US-11-074-176-110
; Sequence 110, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaeshammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Perill, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-110

Query Match 84.8%; Score 28; DB 7; Length 582;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YWIG 5
|||
Db 128 YWIG 131

RESULT 14

US-10-821-234-1253
; Sequence 1253, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt seq_genes Version 1.0
; SEQ ID NO 1253
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1253

Query Match 81.8%; Score 27; DB 6; Length 117;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YWIG 5
|||
Db 68 YWIG 71

RESULT 15

US-11-108-172-1110
; Sequence 1110, Application US/11108172
; Publication No. US20050260177A1
; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stoik, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C15
; CURRENT APPLICATION NUMBER: US/11/108,172
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 10/025,380
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 09/922,217
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 09/833,263
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 09/649,811
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 09/609,448
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/575,251
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/519,444
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/504,629
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: US 09/480,321
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: US 09/476,296
; PRIOR FILING DATE: 1999-12-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1110
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-108-172-1110

Query Match 81.8%; Score 27; DB 7; Length 314;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWI 4
|||
Db 141 TYWI 144

Search completed: December 3, 2005, 14:17:54
Job time : 0.285714 secs

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OW protein - protein search, using sw model

Run on: December 3, 2005, 14:10:00 ; Search time 29.0735 Seconds
(without alignments)
256.916 Million cell updates/sec

Title: US-10-769-144-14

Perfect score: 92

Sequence: 1 IIPGDSDTIYSPSQG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	17	ADR46831	Adr46831 Human ant
2	92	100.0	116	Aam48005	Aam48005 Human mon
3	92	100.0	116	ADR46821	Adr46821 Human ant
4	92	100.0	411	ADR46829	Adr46829 Human p91
5	92	100.0	468	ADR46819	Adr46819 Human ant
6	92	100.0	613	ADR46827	Adr46827 Human bet
7	88	95.7	247	ADR28066	Adr28066 NPB polyp
8	85	92.4	17	ABR01560	ABR01560 Human ant
9	85	92.4	17	ABU08151	ABU08151 ErbB2 rec
10	85	92.4	17	ADD69218	ADD69218 Human hea
11	85	92.4	17	ADD69224	ADD69224 Human hea
12	85	92.4	17	ADD69221	ADD69221 Human hea
13	85	92.4	17	ADD69227	ADD69227 Human hea
14	85	92.4	17	ADD69230	ADD69230 Human hea
15	85	92.4	17	ADH89396	ADH89396 Human tra
16	85	92.4	17	ADP47140	ADP47140 Human pho
17	85	92.4	17	ADP47176	ADP47176 Human pho
18	85	92.4	17	ADP47158	ADP47158 Human pho
19	85	92.4	17	ADP47173	ADP47173 Human pho
20	85	92.4	17	ADS87942	ADS87942 Anti-IFN-
21	85	92.4	17	ADS94939	ADS94939 Anti-IFN-
22	85	92.4	17	ADR69906	ADR69906 Human IL-
23	85	92.4	17	ADX15527	ADX15527 Human ant
24	85	92.4	17	ADY26778	ADY26778 Human ant

25	85	92.4	17	9	AEA18876	Aea18876 Amino aci
26	85	92.4	84	2	AAW62797	Aaw62797 Amino aci
27	85	92.4	98	2	AAW54008	Aaw54008 Human ant
28	85	92.4	98	5	ABG78233	Abg78233 Human Fv
29	85	92.4	98	5	ABG78231	Abg78231 Human Fv
30	85	92.4	98	5	ABG78232	Abg78232 Human Fv
31	85	92.4	98	5	ABG91924	Abg91924 Human ant
32	85	92.4	98	5	ABG91922	Abg91922 Human ant
33	85	92.4	98	5	ABG91923	Abg91923 Human ant
34	85	92.4	98	6	ABU56809	Abu56809 Human Imm
35	85	92.4	98	6	ABP56508	Abp56508 Human ant
36	85	92.4	98	6	ABJ18687	Abj18687 Antibody
37	85	92.4	98	6	ABO27112	ABO27112 Human ger
38	85	92.4	98	7	ADD69247	Add69247 Human hea
39	85	92.4	98	7	ADF10156	Adf10156 Antibody
40	85	92.4	98	7	ADF09948	Adf09948 Antibody
41	85	92.4	98	7	ADF10053	Adf10053 VEGF anti
42	85	92.4	98	7	ADK18943	Adk18943 Anti-huma
43	85	92.4	98	7	ADK18888	Adk18888 Anti-huma
44	85	92.4	98	7	ADK18877	Adk18877 Anti-huma
45	85	92.4	98	7	ADK18878	Adk18878 Anti-huma

ALIGNMENTS

RESULT 1

ADR46831

ID ADR46831 standard; peptide; 17 AA.

XX AC ADR46831;

XX DT 18-NOV-2004 (first entry)

XX DE Human antibody B11 heavy chain variable region CDR2 SEQ ID NO:14.

XX KW molecular conjugate; monoclonal antibody; human antigen presenting cell;
KW antigen presenting cell; APC; human; beta human chorionic gonadotropin;
KW betahCG; beta chorionic gonadotropin; antibody;
KW T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
KW immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
KW CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
KW melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
KW antibody B11; heavy chain variable region; CDR;
KW complementarity determining region.

XX OS Homo sapiens.

XX PN WO2004074432-A2.

XX PD 02-SEP-2004.

XX PF 30-JAN-2004; 2004WO-US002725.

XX PR 31-JAN-2003; 2003US-0443979P.

XX PA (MEDA-) MEDAREX INC.

XX PI Keler T, Endres M, He L, Ramakrishna V;

XX DR WPI; 2004-635555/61.

XX PT New molecular conjugate having a monoclonal antibody that binds to human APCs linked to a beta human chorionic gonadotropin, useful for inducing a cytotoxic T cell response in cancers and infectious diseases.

XX PS Claim 8; SEQ ID NO 14; 82pp; English.

XX CC The present invention describes a molecular conjugate comprising a monoclonal antibody that binds to human antigen presenting cells (APCs) linked to beta human chorionic gonadotropin (betahCG), where the antibody comprises a heavy and/or light chain variable region derived from a human VH5-51 or Vk-L15 germline sequence with the 98 or 95 amino acid sequences

of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also described: (1) a molecular conjugate comprising a human antibody heavy chain and a human antibody light chain, where either or both chains are linked to betaHCG; (2) a molecular conjugate comprising a human single chain antibody that binds to human APCs linked to betaHCG, where the conjugate comprises the 411 amino acid sequence of SEQ ID NO:12 (ADR46829); (3) a composition comprising any of the molecular conjugates as described above, and a carrier, optionally in combination with an adjuvant; (4) inducing or enhancing a T cell-mediated immune response, against betaHCG, comprising contacting any of the molecular conjugates described above with APCs such that the antigen is processed and presented to T cells in a manner which induces or enhances a T cell-mediated response against the antigen; (5) immunising a subject comprising administering any of the molecular conjugates described above, optionally in combination with an adjuvant, a cytokine which stimulates proliferation of dendritic cells and/or an immunostimulatory agent; and (6) inducing or enhancing a cytotoxic T cell response against an antigen, comprising forming a conjugate of the antigen and a monoclonal antibody which binds to APCs, and contacting the conjugate either in vivo or ex vivo with APCs such that the antigen is internalised, processed and presented to T cells in a manner which induces or enhances a cytotoxic T cell response against the antigen. The molecular conjugate has cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic, virucide and antimalarial activities, and can be used as a CD8 agonist, and in vaccines. The methods and compositions of the present invention are useful for inducing a cytotoxic T cell response, and in particular for treating autoimmune disorders, cancers and infectious diseases by eliciting a potent antigen-specific cytotoxic T lymphocyte response, including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and herpes. The present sequence represents the human antibody B11 heavy chain variable region complementarity determining region 2 (CDR2) amino acid sequence, which is used in the exemplification of the present invention.

Sequence 17 AA;

Query Match 100.0%; Score 92; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTIYSPSFQ 17
| | | | | | | | | | | | | | | | |
Db 1 IIYPGDSDTIYSPSFQ 17

RESULT 2
AAM48005
ID AAM48005 standard; protein; 116 AA.

XX AC AAM48005;

XX DT 08-MAR-2002 (first entry)

XX DE Human monoclonal antibody B11 variable heavy chain protein.

XX KW Human; monoclonal antibody; B11; antigen binding portion; dendritic cell; mannose receptor; growth; cytotoxicity; pathogen; virus; bacterium; autoimmune disease; inflammatory disorder; rheumatoid arthritis; multiple sclerosis; diabetes mellitus; immunomodulatory; anti-inflammatory; antirheumatic; antidiabetic; neuroprotective; antidiabetic; antianaemic; endocrine; dermatological; antithyroid; uropathic; ophthalmological; muscular.

XX OS Homo sapiens.

XX PN WO200185798-A2.

XX PD 15-NOV-2001.

XX PF 08-MAY-2001; 2001WO-US015114.

XX PR 08-MAY-2000; 2000US-0203126P.

XX PR 07-SEP-2000; 2000US-0230739P.

XX PA (MEDA-) MEDAREX INC.
XX PI Deo YM, Keler T;
XX WPI; 2002-089788/12.
XX N-PSDB; ABA05500.

XX New human monoclonal antibodies specific for dendritic cells, useful for inhibiting growth or inducing cytotoxicity of a dendritic cell and treating or preventing a dendritic cell mediated disease, e.g., autoimmune disorders.

XX Example 2; Fig 13; 95pp; English.

XX The invention relates to human monoclonal antibodies or their antigen binding portions that specifically bind to dendritic cells and has one or more of the following characteristics: (a) a binding affinity constant to a dendritic cell of at least about 10 to the power 7 M-1; (b) the ability to opsonise a dendritic cell; (c) the ability to internalise after binding to dendritic cells; or (d) the ability to activate dendritic cells. The isolated human monoclonal antibody or its antigen binding portion may also have any of the following characteristics: (a) mediates cytotoxicity of dendritic cells in the presence of human effector cells; or (b) inhibits growth of dendritic cells. The antibodies or its antigen binding portion, binds to and blocks the human mannose receptor on dendritic cells. The antibodies have immunomodulatory, anti-inflammatory, antirheumatic, antithyroid, neuroprotective, antidiabetic, antianaemic, endocrine, dermatological, antithyroid, uropathic, ophthalmological and muscular activity. The antibodies or their antigen-binding fragments are useful for inhibiting growth of a dendritic cell, inducing cytotoxicity of a dendritic cell, treating or preventing a dendritic cell mediated disease, detecting the presence of a dendritic cell, targeting an antigen to a dendritic cell and preventing binding of a pathogen (a virus or a bacterium) to human mannose receptor on dendritic cells. In particular, the antibodies may be used to treat autoimmune diseases, graft versus host disease, immune system or inflammatory disorders (e.g. rheumatoid arthritis), multiple sclerosis, diabetes mellitus, myasthenia gravis, pernicious anaemia, Addison's disease, lupus erythematosus, Reiter's syndrome and Graves disease. The present sequence is that of the human monoclonal antibody B11 variable heavy chain, useful to the invention

Sequence 116 AA;

Query Match 100.0%; Score 92; DB 5; Length 116;

Best Local Similarity 100.0%; Pred. No. 4.3e-06;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTIYSPSFQ 17
| | | | | | | | | | | | | | | | |
Db 50 IIYPGDSDTIYSPSFQ 66

RESULT 3

AD46821

ID ADR46821 standard; protein; 116 AA.

XX AC ADR46821;

XX DT 18-NOV-2004 (first entry)

XX DE Human antibody B11 heavy chain variable region protein SEQ ID NO:4.

XX KW molecular conjugate; monoclonal antibody; human antigen presenting cell; antigen presenting cell; APC; human; beta human chorionic gonadotropin; betaHCG; beta chorionic gonadotropin; antibody; T cell-mediated immune response; immunisation; cytostatic; antimicrobial; immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial; CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease; melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes; antibody B11; heavy chain variable region.

XX OS Homo sapiens.

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XX WO2004074432-A2.
XX
XX
XX PD 02-SEP-2004.
XX
XX PF 30-JAN-2004; 2004WO-US002725.
XX
XX PR 31-JAN-2003; 2003US-0443979P.
XX
XX PA (MEDA-) MEDAREX INC.
XX
XX PI Keler T, Endres M, He L, Ramakrishna V;
XX
XX WPI; 2004-635555/61.
XX
XX DR N-PSDB; ADR46820.
XX
XX
XX PT New molecular conjugate having a monoclonal antibody that binds to human
XX APCs linked to a beta human chorionic gonadotropin, useful for inducing a
XX cytotoxic T-cell response in cancers and infectious diseases.
XX
XX PS Claim 11; SEQ ID NO 4; 82pp; English.
XX
XX
XX CC The present invention describes a molecular conjugate comprising a
XX monoclonal antibody that binds to human antigen presenting cells (APCs)
XX linked to beta human chorionic gonadotropin (betahCG), where the antibody
XX comprises a heavy and/or light chain variable region derived from a human
XX VH5-51 or Vκ-L15 germline sequence with the 98 or 95 amino acid sequences
XX of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
XX described: (1) a molecular conjugate comprising a human antibody heavy
XX chain and a human antibody light chain, where either or both chains are
XX linked to betahCG; (2) a molecular conjugate comprising a human single
XX chain antibody that binds to human APCs linked to betahCG, where the
XX conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
XX (ADR46829); (3) a composition comprising any of the molecular conjugates
XX as described above, and a carrier, optionally in combination with an
XX adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
XX against betahCG, comprising contacting any of the molecular conjugates
XX described above with APCs such that the antigen is processed and
XX presented to T cells in a manner which induces or enhances a T cell-
XX mediated response against the antigen; (5) immunising a subject
XX comprising administering any of the molecular conjugates described above,
XX optionally in combination with an adjuvant, a cytokine which stimulates
XX proliferation of dendritic cells and/or an immunostimulatory agent; and
XX (6) inducing or enhancing a cytotoxic T cell response against an antigen,
XX comprising forming a conjugate of the antigen and a monoclonal antibody
XX which binds to APCs, and contacting the conjugate either in vivo or ex
XX vivo with APCs such that the antigen is internalised, processed and
XX cell response against the antigen. The molecular conjugate has
XX cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
XX virucide and antimalarial activities, and can be used as a CD8 agonist,
XX and in vaccines. The methods and compositions of the present invention
XX are useful for inducing a cytotoxic T cell response, and in particular
XX eliciting a potent antigen-specific cytotoxic T lymphocyte response,
XX including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
XX herpes. The present sequence represents a human antibody B11 heavy chain
XX variable region, which is used in the exemplification of the present
XX invention.
XX
XX SQ Sequence 116 AA;
XX
XX Query Match 100.0%; Score 92; DB 8; Length 116;
XX Best Local Similarity 100.0%; Pred. No. 4.3e-06;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 IYPGSDTIYSPSQ 17
XX |||||||||||||||
XX Db 50 IYPGSDTIYSPSQ 66
XX
XX RESULT 4
XX ADR46829

```

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ID
XX
XX AC ADR46829;
XX
XX DT 18-NOV-2004 (first entry)
XX
XX DE Human pB11-betahCG molecular conjugate protein SEQ ID NO:12.
XX
XX KW molecular conjugate; monoclonal antibody; human antigen presenting cell;
XX antigen presenting cell; APC; human; beta human chorionic gonadotropin;
XX betahCG; beta chorionic gonadotropin; antibody;
XX T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
XX immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
XX CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
XX melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
XX antibody B11; pB11-betahCG molecular conjugate; fusion protein.
XX
XX OS Homo sapiens.
XX
XX OS Synthetic.
XX
XX PN WO2004074432-A2.
XX
XX PD 02-SEP-2004.
XX
XX PF 30-JAN-2004; 2004WO-US002725.
XX
XX PR 31-JAN-2003; 2003US-0443979P.
XX
XX PA (MEDA-) MEDAREX INC.
XX
XX PI Keler T, Endres M, He L, Ramakrishna V;
XX
XX WPI; 2004-635555/61.
XX
XX DR N-PSDB; ADR46828.
XX
XX PT New molecular conjugate having a monoclonal antibody that binds to human
XX APCs linked to a beta human chorionic gonadotropin, useful for inducing a
XX cytotoxic T cell response in cancers and infectious diseases.
XX
XX PS Claim 16; SEQ ID NO 12; 82pp; English.
XX
XX CC The present invention describes a molecular conjugate comprising a
XX monoclonal antibody that binds to human antigen presenting cells (APCs)
XX linked to beta human chorionic gonadotropin (betahCG), where the antibody
XX comprises a heavy and/or light chain variable region derived from a human
XX VH5-51 or Vκ-L15 germline sequence with the 98 or 95 amino acid sequences
XX of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
XX described: (1) a molecular conjugate comprising a human antibody heavy
XX chain and a human antibody light chain, where either or both chains are
XX linked to betahCG; (2) a molecular conjugate comprising a human single
XX chain antibody that binds to human APCs linked to betahCG, where the
XX conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
XX (ADR46829); (3) a composition comprising any of the molecular conjugates
XX as described above, and a carrier, optionally in combination with an
XX adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
XX against betahCG, comprising contacting any of the molecular conjugates
XX described above with APCs such that the antigen is processed and
XX presented to T cells in a manner which induces or enhances a T cell-
XX mediated response against the antigen; (5) immunising a subject
XX comprising administering any of the molecular conjugates described above,
XX optionally in combination with an adjuvant, a cytokine which stimulates
XX proliferation of dendritic cells and/or an immunostimulatory agent; and
XX (6) inducing or enhancing a cytotoxic T cell response against an antigen,
XX comprising forming a conjugate of the antigen and a monoclonal antibody
XX which binds to APCs, and contacting the conjugate either in vivo or ex
XX vivo with APCs such that the antigen is internalised, processed and
XX cell response against the antigen. The molecular conjugate has
XX cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
XX virucide and antimalarial activities, and can be used as a CD8 agonist,
XX and in vaccines. The methods and compositions of the present invention
XX are useful for inducing a cytotoxic T cell response, and in particular
XX eliciting a potent antigen-specific cytotoxic T lymphocyte response,
XX including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
XX herpes. The present sequence represents a human antibody B11 heavy chain
XX variable region, which is used in the exemplification of the present
XX invention.
XX
XX SQ Sequence 116 AA;
XX
XX Query Match 100.0%; Score 92; DB 8; Length 116;
XX Best Local Similarity 100.0%; Pred. No. 4.3e-06;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 IYPGSDTIYSPSQ 17
XX |||||||||||||||
XX Db 50 IYPGSDTIYSPSQ 66
XX
XX RESULT 4
XX ADR46829

```

CC eliciting a potent antigen-specific cytotoxic T lymphocyte response,
 CC including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
 CC herpes. The present sequence represents a human pbl1-betahCG molecular
 CC conjugate, which is used in the exemplification of the present invention.

XX SQ Sequence 411 AA;

Query Match 100.0%; Score 92; DB 8; Length 411;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IYIPGDSDTIYSPSFQ 17
 |||||
 Db 191 IYIPGDSDTIYSPSFQ 207

RESULT 5

ADRA46819
 ID ADRA46819 standard; protein; 468 AA.

AC ADRA46819;

XX 18-NOV-2004 (first entry)

XX Human antibody B11 heavy chain variable region protein SEQ ID NO:2.

XX molecular conjugate; monoclonal antibody; human antigen presenting cell;
 KW antigen presenting cell; APC; human; beta human chorionic gonadotropin;
 KW betahCG; beta chorionic gonadotropin; antibody;
 KW T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
 KW immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
 KW CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
 KW melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
 KW antibody B11; heavy chain variable region.

XX Homo sapiens.

XX WO2004074432-A2.

XX 02-SEP-2004.

XX 30-JAN-2004; 2004WO-US002725.

XX 31-JAN-2003; 2003US-0443979P.

XX (MEDA-) MEDAREX INC.

XX Keler T, Endres M, He L, Ramakrishna V;

XX WPI; 2004-635555/61.

XX N-PSDB; ADRA46818.

XX New molecular conjugate having a monoclonal antibody that binds to human
 PT APCs linked to a beta human chorionic gonadotropin, useful for inducing a
 PT cytotoxic T cell response in cancers and infectious diseases.

XX Claim 13; SEQ ID NO 2; 82pp; English.

XX The present invention describes a molecular conjugate comprising a
 CC monoclonal antibody that binds to human antigen presenting cells (APCs)
 CC linked to beta human chorionic gonadotropin (betahCG), where the antibody
 CC comprises a heavy and/or light chain variable region derived from a human
 CC VH5-51 or Vh-L15 germline sequence with the 98 or 95 amino acid sequences
 CC of SEQ ID NO:30 or 32 (ADRA46847, or ADRA46849), respectively. Also
 CC described: (1) a molecular conjugate comprising a human antibody heavy
 CC chain and a human antibody light chain, where either or both chains are
 CC linked to betahCG; (2) a molecular conjugate comprising a human single
 CC chain antibody that binds to human APCs linked to betahCG, where the
 CC conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
 CC (ADRA46829); (3) a composition comprising any of the molecular conjugates
 CC as described above, and a carrier, optionally in combination with an
 CC adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
 CC against betahCG, comprising contacting any of the molecular conjugates

CC described above with APCs such that the antigen is processed and
 CC presented to T cells in a manner which induces or enhances a T cell-
 CC mediated response against the antigen; (5) immunising a subject
 CC comprising administering any of the molecular conjugates described above,
 CC optionally in combination with an adjuvant, a cytokine which stimulates
 CC proliferation of dendritic cells and/or an immunostimulatory agent; and
 CC (6) inducing or enhancing a cytotoxic T cell response against an antigen,
 CC comprising forming a conjugate of the antigen and a monoclonal antibody
 CC which binds to APCs, and contacting the conjugate either in vivo or ex
 CC vivo with APCs such that the antigen is internalised, processed and
 CC presented to T cells in a manner which induces or enhances a cytotoxic T
 CC cell response against the antigen. The molecular conjugate has
 CC cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
 CC virucide and antimalarial activities, and can be used as a CD8 agonist,
 CC and in vaccines. The methods and compositions of the present invention
 CC are useful for inducing a cytotoxic T cell response, and in particular
 CC for treating autoimmune disorders, cancers and infectious diseases by
 CC eliciting a potent antigen-specific cytotoxic T lymphocyte response,
 CC including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
 CC herpes. The present sequence represents a human antibody B11 heavy chain
 CC variable region, which is used in the exemplification of the present
 CC invention.

XX SQ Sequence 468 AA;

Query Match 100.0%; Score 92; DB 8; Length 468;
 Best Local Similarity 100.0%; Pred. No. 1.8e-05;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IYIPGDSDTIYSPSFQ 17
 |||||
 Db 69 IYIPGDSDTIYSPSFQ 85

RESULT 6

ADRA46827

ID ADRA46827 standard; protein; 613 AA.

XX AC ADRA46827;

XX 18-NOV-2004 (first entry)

XX Human betahCG-B11 molecular conjugate protein SEQ ID NO:10.

XX molecular conjugate; monoclonal antibody; human antigen presenting cell;
 KW antigen presenting cell; APC; human; beta human chorionic gonadotropin;
 KW betahCG; beta chorionic gonadotropin; antibody;
 KW T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
 KW immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
 KW CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
 KW melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
 KW antibody B11; betahCG-B11 molecular conjugate; fusion protein.

XX Homo sapiens.

XX Synthetic.

XX WO2004074432-A2.

XX 02-SEP-2004.

XX 30-JAN-2004; 2004WO-US002725.

XX 31-JAN-2003; 2003US-0443979P.

XX (MEDA-) MEDAREX INC.

XX Keler T, Endres M, He L, Ramakrishna V;

XX WPI; 2004-635555/61.

XX N-PSDB; ADRA46826.

XX New molecular conjugate having a monoclonal antibody that binds to human
 PT APCs linked to a beta human chorionic gonadotropin, useful for inducing a

PT cytotoxic T cell response in cancers and infectious diseases.

PS Example 1; SEQ ID NO 10; 82pp; English.

XX The present invention describes a molecular conjugate comprising a
 CC monoclonal antibody that binds to human antigen presenting cells (APCs)
 CC linked to beta human chorionic gonadotropin (betahCG), where the antibody
 CC comprises a heavy and/or light chain variable region derived from a human
 CC VH5-51 or Vh-115 germline sequence with the 98 or 95 amino acid sequences
 CC of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
 CC described: (1) a molecular conjugate comprising a human antibody heavy
 CC chain and a human antibody light chain, where either or both chains are
 CC linked to betahCG; (2) a molecular conjugate comprising a human single
 CC chain antibody that binds to human APCs linked to betahCG, where the
 CC conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
 CC (ADR46829); (3) a composition comprising any of the molecular conjugates
 CC as described above, and a carrier, optionally in combination with an
 CC adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
 CC against betahCG, comprising contacting any of the molecular conjugates
 CC described above with APCs such that the antigen is processed and
 CC presented to T cells in a manner which induces or enhances a T cell-
 CC mediated response against the antigen; (5) immunising a subject
 CC comprising administering any of the molecular conjugates described above,
 CC optionally in combination with an adjuvant, a cytokine which stimulates
 CC proliferation of dendritic cells and/or an immunostimulatory agent; and
 CC (6) inducing or enhancing a cytotoxic T cell response against an antigen,
 CC comprising forming a conjugate of the antigen and a monoclonal antibody
 CC which binds to APCs, and contacting the conjugate either in vivo or ex
 CC vivo with APCs such that the antigen is internalised, processed and
 CC presented to T cells in a manner which induces or enhances a cytotoxic T
 CC cell response against the antigen. The molecular conjugate has
 CC cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
 CC virucide and antimalarial activities, and can be used as a CD8 agonist,
 CC and in vaccines. The methods and compositions of the present invention
 CC are useful for inducing a cytotoxic T cell response, and in particular
 CC for treating autoimmune disorders, cancers and infectious diseases by
 CC eliciting a potent antigen-specific cytotoxic T lymphocyte response,
 CC including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
 CC herpes. The present sequence represents a human betahCG-B11 molecular
 CC conjugate, which is used in the exemplification of the present invention.

XX Sequence 613 AA;

Query Match 100.0%; Score 92; DB 8; Length 613;
 Best Local Similarity 100.0%; Pred. No. 2.3e-05;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYPGSDSTIYSPSQG 17
 |||||
 Db 69 IYPGSDSTIYSPSQG 85

RESULT 7
 ADR28066
 ID ADR28066 standard; protein; 247 AA.

XX ADR28066;

DT 07-OCT-2004 (first entry)

DE NPB polypeptide scFv11, seq id 13.

KW Cytostatic; metastasis inhibitor; neuropilin binder; NPB; scFv;
 KW single chain antibody; neuropilin-1; NP-1; angiogenesis; tumour; cancer.

XX Mus sp.
 OS Synthetic.

XX Key Location/Qualifiers
 FH 89..105
 FT /note= "complementary determining region claimed under
 FT claim 5"
 XX

PN WO2004056874-A2.

PD 08-JUL-2004.

XX 22-DEC-2003; 2003WO-EP014756.

XX 20-DEC-2002; 2002US-0435893P.

PR 15-JAN-2003; 2003EP-00000615.

XX (XERI-) XERION PHARM AG.
 PA (TUFT) UNIV TUFTS.

XX Unger CM, Beste G, Zehetmeier C, Lain B, Torella C, Niewoehner J;
 PI Jay DG, Eustace BK, Knauer R, Jensen KH;

XX WPI; 2004-507700/48.

DR N-PSDB; ADR28100.

XX Novel neuropilin binder which is scFv, antibody fragment or bioconjugate,
 PT that modulates neuropilin-1 function or inhibits NP-1 dependent
 PT angiogenesis of endothelial cells and/or invasion of tumor cells useful
 PT for treating cancer.

XX Claim 3; SEQ ID NO 13; 120pp; English.

XX The invention relates to a neuropilin binder (NPB) (I) which is a
 CC polypeptide, antibody, scFv, antibody fragment or bioconjugate, that
 CC modulates neuropilin-1 (NP-1) function or inhibits NP-1 dependent
 CC angiogenesis of endothelial cells and/or invasion of tumour cells,
 CC whereby the NPB binds to NP-1 and modulates NP-1 function. Further
 CC disclosed is an ex vivo method of determining the dependency of the
 CC invasiveness of a naturally occurring invasive cancer cell on the
 CC functionality of NP-1. The NPB of the invention is an inhibitor of
 CC metastasis of NP-1 mediated invasion and/or adhesion and an inhibitor of
 CC tumour-associated NP-1 dependent angiogenesis. The NPB of the invention
 CC is useful for detecting NP-1 expression, modulation of NP-1 function,
 CC particularly modulation or inhibition of NP-dependent invasion or
 CC adhesion of cells, preferably tumour cells. It is useful in the
 CC manufacture of medicament for the treatment or prevention of NP-dependent
 CC angiogenesis and non-physiological blood vessel growth, particularly
 CC correlated with a tumour. It is also useful for treatment or prevention
 CC of cancer and/or metastasis of tumour cells. The current sequence
 CC represents a single chain antibody neuropilin binder (NPB) polypeptide.

XX Sequence 247 AA;

Query Match 95.7%; Score 88; DB 8; Length 247;
 Best Local Similarity 94.1%; Pred. No. 3.8e-05;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYPGSDSTIYSPSQG 17
 |||||
 Db 40 IYPGSDSTIYSPSQG 56

RESULT 8

ABR01560

ID ABR01560 standard; peptide; 17 AA.

XX ABR01560;

XX 16-APR-2003 (first entry)

XX Human anti-TIMP-1 Fab VLCDR3 #48.

XX Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3;
 KW matrix metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic;
 KW variable light chain; cytotatic; nephrotropic; cardiant; liver fibrosis;
 KW alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;
 KW lupus nephritis; glomerulosclerotic renal disease; lung cancer;
 KW idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.
 XX Homo sapiens.

XX New isolated human monoclonal antibody comprising a human heavy chain and
PT a human light chain variable regions, both comprising FR1, CDR1, FR2,
PT CDR2, FR3, CDR3 and FR4 sequences, useful for treating or preventing
PT cancer.
XX
PS Claim 2; SEQ ID NO 22; 136pp; English.
XX
XX The invention relates to a novel isolated human monoclonal antibody
CC comprising a human heavy chain variable region and a human light chain
CC variable region both comprising FR (framework region)-1, CDR
CC (complementarity determining region)-1, FR2, CDR2, FR3, CDR3 and FR4
CC sequences. The antibody is directed against the human prostate specific
CC membrane antigen (PSMA). The monoclonal antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating or
CC preventing a disease characterised by the growth of tumour cells such as
CC cancer, particularly prostate cancer, colon cancer or renal carcinoma, as
CC well as doing gene therapy procedures. The current sequence is that of
CC the human heavy chain variable region CDR2 peptide of the invention.
XX
SQ Sequence 17 AA;
Query Match 92.4%; Score 85; DB 7; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.1e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 IYFGDSDTIYSPSQFQ 17
Db 1 IYFGDSDTIYSPSQFQ 17
RESULT 11
ADD69224
ID ADD69224 standard; peptide; 17 AA.
XX
AC ADD69224;
XX
XX 15-JAN-2004 (first entry)
XX
XX Human heavy chain variable region CDR2 peptide - SEQ ID 28.
XX
XX monoclonal antibody; heavy chain variable region; light; framework;
KW complementarity determining; CDR1; FR1; FR2; CDR2; FR3; CDR3; FR4;
KW prostate specific membrane antigen; PSMA; cytostatic; tumour;
KW colon cancer; renal carcinoma; gene therapy; human.
XX
OS Homo sapiens.
XX
XX WO2003064606-A2.
XX
XX 07-AUG-2003.
XX
XX 28-JAN-2003; 2003WO-US002448.
XX
XX 28-JAN-2002; 2002US-00059989.
XX
XX (MEDA-) MEDAREX INC.
XX
XX Deo YM, Graziano R, Hudson D, Holmes EH, Tino WT, Black A;
XX
XX WPI; 2003-618360/58.
XX
XX New isolated human monoclonal antibody comprising a human heavy chain and
PT a human light chain variable regions, both comprising FR1, CDR1, FR2,
PT CDR2, FR3, CDR3 and FR4 sequences, useful for treating or preventing
PT cancer.
XX
PS Claim 2; SEQ ID NO 28; 136pp; English.
XX
XX The invention relates to a novel isolated human monoclonal antibody
CC comprising a human heavy chain variable region and a human light chain
CC variable region both comprising FR (framework region)-1, CDR
CC (complementarity determining region)-1, FR2, CDR2, FR3, CDR3 and FR4

CC sequences. The antibody is directed against the human prostate specific
CC membrane antigen (PSMA). The monoclonal antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating or
CC preventing a disease characterised by the growth of tumour cells such as
CC cancer, particularly prostate cancer, colon cancer or renal carcinoma, as
CC well as doing gene therapy procedures. The current sequence is that of
CC the human heavy chain variable region CDR2 peptide of the invention.
XX
SQ Sequence 17 AA;
Query Match 92.4%; Score 85; DB 7; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.1e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 IYFGDSDTIYSPSQFQ 17
Db 1 IYFGDSDTIYSPSQFQ 17
RESULT 12
ADD69221
ID ADD69221 standard; peptide; 17 AA.
XX
AC ADD69221;
XX
XX 15-JAN-2004 (first entry)
XX
XX Human heavy chain variable region CDR2 peptide - SEQ ID 25.
XX
XX monoclonal antibody; heavy chain variable region; light; framework;
KW complementarity determining; CDR1; FR1; FR2; CDR2; FR3; CDR3; FR4;
KW prostate specific membrane antigen; PSMA; cytostatic; tumour;
KW colon cancer; renal carcinoma; gene therapy; human.
XX
OS Homo sapiens.
XX
XX WO2003064606-A2.
XX
XX 07-AUG-2003.
XX
XX 28-JAN-2003; 2003WO-US002448.
XX
XX 28-JAN-2002; 2002US-00059989.
XX
XX (MEDA-) MEDAREX INC.
XX
XX Deo YM, Graziano R, Hudson D, Holmes EH, Tino WT, Black A;
XX
XX WPI; 2003-618360/58.
XX
XX New isolated human monoclonal antibody comprising a human heavy chain and
PT a human light chain variable regions, both comprising FR1, CDR1, FR2,
PT CDR2, FR3, CDR3 and FR4 sequences, useful for treating or preventing
PT cancer.
XX
PS Claim 2; SEQ ID NO 25; 136pp; English.
XX
XX The invention relates to a novel isolated human monoclonal antibody
CC comprising a human heavy chain variable region and a human light chain
CC variable region both comprising FR (framework region)-1, CDR
CC (complementarity determining region)-1, FR2, CDR2, FR3, CDR3 and FR4
CC sequences. The antibody is directed against the human prostate specific
CC membrane antigen (PSMA). The monoclonal antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating or
CC preventing a disease characterised by the growth of tumour cells such as
CC cancer, particularly prostate cancer, colon cancer or renal carcinoma, as
CC well as doing gene therapy procedures. The current sequence is that of
CC the human heavy chain variable region CDR2 peptide of the invention.
XX
SQ Sequence 17 AA;
Query Match 92.4%; Score 85; DB 7; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.1e-06;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTYSPSFQ 17
 |||||
 Db 1 IIYPGDSDTYSPSFQ 17
 |||||

RESULT 13
 ADD69227 standard; peptide; 17 AA.
 XX
 AC ADD69227;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Human heavy chain variable region CDR2 peptide - SEQ ID 31.
 XX
 KW monoclonal antibody; heavy chain variable region; light; framework;
 KW complementarity determining; CDR1; FR1; FR2; CDR2; FR3; CDR3; FR4;
 KW prostate specific membrane antigen; PSMA; cytostatic; tumour;
 KW colon cancer; renal carcinoma; gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 FN WO2003064606-A2.
 XX
 PD 07-AUG-2003.
 XX
 PF 28-JAN-2003; 2003WO-US002448.
 XX
 PP 28-JAN-2003; 2003WO-US002448.
 XX
 PR 28-JAN-2002; 2002US-00059989.
 XX
 PA (MEDA-) MEDAREX INC.
 XX
 PI Deo YM, Graziano R, Hudson D, Holmes EH, Tino WT, Black A;
 XX
 DR WPI; 2003-618360/58.
 XX
 CC New isolated human monoclonal antibody comprising a human heavy chain and
 PT a human light chain variable regions, both comprising FR1, CDR1, FR2,
 PT CDR2, FR3, CDR3 and FR4 sequences, useful for treating or preventing
 PT cancer.
 XX
 PS Claim 2; SEQ ID NO 31; 136pp; English.
 XX
 CC The invention relates to a novel isolated human monoclonal antibody
 CC comprising a human heavy chain variable region and a human light chain
 CC variable region both comprising FR (framework region)-1, CDR
 CC (complementarity determining region)-1, FR2, CDR2, FR3, CDR3 and FR4
 CC sequences. The antibody is directed against the human prostate specific
 CC membrane antigen (PSMA). The monoclonal antibody of the invention
 CC demonstrates cytostatic activity and may be useful for treating or
 CC preventing a disease characterised by the growth of tumour cells such as
 CC cancer, particularly prostate cancer, colon cancer or renal carcinoma, as
 CC well as during gene therapy procedures. The current sequence is that of
 CC the human heavy chain variable region CDR2 peptide of the invention.
 XX
 SQ Sequence 17 AA;
 Query Match 92.4%; Score 85; DB 7; Length 17;
 Best Local Similarity 94.1%; Pred. No. 7.1e-06;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTYSPSFQ 17
 |||||
 Db 1 IIYPGDSDTYSPSFQ 17
 |||||

RESULT 14
 ADD69230 standard; peptide; 17 AA.
 XX
 AC ADD69230;
 XX

XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Human heavy chain variable region CDR2 peptide - SEQ ID 34.
 XX
 KW monoclonal antibody; heavy chain variable region; light; framework;
 KW complementarity determining; CDR1; FR1; FR2; CDR2; FR3; CDR3; FR4;
 KW prostate specific membrane antigen; PSMA; cytostatic; tumour;
 KW colon cancer; renal carcinoma; gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 FN WO2003064606-A2.
 XX
 PD 07-AUG-2003.
 XX
 PF 28-JAN-2003; 2003WO-US002448.
 XX
 PP 28-JAN-2002; 2002US-00059989.
 XX
 PA (MEDA-) MEDAREX INC.
 XX
 PI Deo YM, Graziano R, Hudson D, Holmes EH, Tino WT, Black A;
 XX
 DR WPI; 2003-618360/58.
 XX
 CC New isolated human monoclonal antibody comprising a human heavy chain and
 PT a human light chain variable regions, both comprising FR1, CDR1, FR2,
 PT CDR2, FR3, CDR3 and FR4 sequences, useful for treating or preventing
 PT cancer.
 XX
 PS Claim 2; SEQ ID NO 34; 136pp; English.
 XX
 CC The invention relates to a novel isolated human monoclonal antibody
 CC comprising a human heavy chain variable region and a human light chain
 CC variable region both comprising FR (framework region)-1, CDR
 CC (complementarity determining region)-1, FR2, CDR2, FR3, CDR3 and FR4
 CC sequences. The antibody is directed against the human prostate specific
 CC membrane antigen (PSMA). The monoclonal antibody of the invention
 CC demonstrates cytostatic activity and may be useful for treating or
 CC preventing a disease characterised by the growth of tumour cells such as
 CC cancer, particularly prostate cancer, colon cancer or renal carcinoma, as
 CC well as during gene therapy procedures. The current sequence is that of
 CC the human heavy chain variable region CDR2 peptide of the invention.
 XX
 SQ Sequence 17 AA;
 Query Match 92.4%; Score 85; DB 7; Length 17;
 Best Local Similarity 94.1%; Pred. No. 7.1e-06;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTYSPSFQ 17
 |||||
 Db 1 IIYPGDSDTYSPSFQ 17
 |||||

RESULT 15
 ADH89396 standard; peptide; 17 AA.
 XX
 AC ADH89396;
 XX
 DT 15-APR-2004 (first entry)
 XX
 DE Human transferrin fusion protein-related CDR2 peptide SeqID40.
 XX
 KW fusion protein; transferrin protein; glycosylation;
 KW antibody variable region; cytostatic; antibacterial; virucide;
 KW antiparasitic; immunosuppressive; antiarthritic; gene therapy;
 KW septic shock; endotoxin shock; cachexia syndrome; bacterial infection;
 KW viral infection; parasitic infection; neoplasm; autoimmune disease;
 KW arthritis; graft rejection.
 XX

OS Unidentified.
XX
XX US2003226155-A1.
XX
XX 04-DEC-2003.
XX
XX 10-MAR-2003; 2003US-00384060.
XX
XX 30-AUG-2001; 2001US-0315745P.
XX
XX 30-NOV-2001; 2001US-0334059P.
XX
XX 30-AUG-2002; 2002US-00231149A.
XX
XX 30-AUG-2002; 2002US-0406977P.
XX
XX (BIOR-) BIOREXIS PHARM CORP.
XX
XX Sadeghi H, Prior CP, Turner A;
XX
XX WPI; 2004-022093/02.
XX
XX
XX New fusion protein comprising a transferrin protein exhibiting reduced
PT glycosylation fused to at least one antibody variable region, useful for
PT preparing a composition for treating e.g., septic shock, neoplasm or
PT autoimmune disease.
XX
XX Example 2; SEQ ID NO 40; 82pp; English.
XX
XX This invention relates to a novel fusion protein which comprises a
CC transferrin protein exhibiting reduced glycosylation fused to at least
CC one antibody variable region. The invention may be useful for the
CC development of compounds with cytostatic, antibacterial, virucide,
CC antiparasitic, immunosuppressive or antiarthritic activity. In addition,
CC the sequences disclosed may be useful for gene therapy. The fusion
CC protein is useful for preparing a composition for treating a disease or
CC disease symptom in a patient for example septic shock, endotoxic shock,
CC cachexia syndromes associated with bacterial, viral or parasitic
CC infections, neoplasm, autoimmune disease, arthritis or adverse effects
CC associated with treatment for preventing graft rejection. The present
CC sequence is that of a CDR 2 peptide which was used in the exemplification
XX of the invention.
XX
XX Sequence 17 AA;
SQ
Query Match 92.4%; Score 85; DB 8; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.1e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 IYPGSDTRYSPFQG 17
Db 1 IYPGSDTRYSPFQG 17
Search completed: December 3, 2005, 14:25:05
Job time : 30.0735 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 14:11:59 ; Search time 4.64898 Seconds
(without alignments)
351.837 Million cell updates/sec

Title: US-10-769-144-14

Perfect score: 92

Sequence: 1 IYFGSDTIYSPSFQ 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	92.4	98	PH1274	Ig heavy chain V r
2	85	92.4	98	S26907	Ig heavy chain V r
3	85	92.4	101	S12428	Ig heavy chain V r
4	85	92.4	101	S12424	Ig heavy chain V r
5	85	92.4	102	PH1266	Ig heavy chain V r
6	85	92.4	102	PH1279	Ig heavy chain V r
7	85	92.4	102	PH1281	Ig heavy chain V r
8	85	92.4	102	PH1277	Ig heavy chain V r
9	85	92.4	102	PH1244	Ig heavy chain V r
10	85	92.4	102	PH1267	Ig heavy chain V r
11	85	92.4	102	PH1272	Ig heavy chain V r
12	85	92.4	102	PH1282	Ig heavy chain V r
13	85	92.4	102	PH1248	Ig heavy chain V r
14	85	92.4	102	PH1280	Ig heavy chain V r
15	85	92.4	102	PH1258	Ig heavy chain V r
16	85	92.4	102	PH1264	Ig heavy chain V r
17	85	92.4	102	PH1259	Ig heavy chain V r
18	85	92.4	102	PH1273	Ig heavy chain V r
19	85	92.4	102	PH1249	Ig heavy chain V r
20	85	92.4	102	PH1271	Ig heavy chain V r
21	85	92.4	102	PH1278	Ig heavy chain V r
22	85	92.4	104	B36006	Ig heavy chain V r
23	85	92.4	113	PH1428	Ig heavy chain V r
24	85	92.4	115	PH1557	Ig heavy chain V r
25	85	92.4	117	A28846	Ig heavy chain pre
26	85	92.4	117	S19670	Ig heavy chain V r
27	85	92.4	123	PH1423	Ig heavy chain V r
28	85	92.4	123	S38492	Ig heavy chain - h
29	85	92.4	123	C36006	Ig heavy chain V r

ALIGNMENTS

RESULT 1

PH1274

Ig heavy chain V region (clone PBL5) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH1274

R:Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.

J. Exp. Med. 176, 1073-1081, 1992

A:Title: Extensive and selective mutation of a rearranged VHS gene in human B cell chrom

A:Reference number: PH1232; MUID:93018822; PMID:1402653

A:Accession: PH1274

A:Molecule type: DNA

A:Residues: 1-98 <CAI>

A:Cross-references: UNIPARC:UPI000017683F

A:Experimental source: adult PBL

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 92.4%; Score 85; DB 2; Length 98;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 IYFGSDTIYSPSFQ 17

Db 54 IYFGSDTIYSPSFQ 70

RESULT 2

S26907

Ig heavy chain V region (DP-73) - human

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S26907

R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of v

A:Reference number: S26885; MUID:93021117; PMID:1404388

A:Accession: S26907

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 <TOM>

A:Cross-references: UNIPARC:UPI000011641E; EMBL:Z12373; NID:g32965; PIDN:CAA78243.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 98;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 IYFGSDTIYSPSFQ 17

Db 1 IYFGSDTIYSPSFQ 17

Db 50 IYPGDSDTTRYSPSFQ 66

RESULT 3

S12428
Ig heavy chain V region (5JB) - human
C/Species: Homo sapiens (man)
C/Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C/Accession: S12428
EMBO J. 8, 3741-3748, 1989
R/Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
A/Title: The smaller human V(H) gene families display remarkably little polymorphism.
A/Reference number: S09421; MUID:90059975; PMID:2511001
A/Accession: S12428
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-101 <SAS>
A/Cross-references: UNIPARC:UPI00001165B; EMBL:X56367
A/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;18-101/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 101;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYPGDSDTTRYSPSFQ 17
|||||
Db 53 IYPGDSDTTRYSPSFQ 69

RESULT 4

S12424
Ig heavy chain V region (5) - human
C/Species: Homo sapiens (man)
C/Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 03-Aug-1998
C/Accession: S12424; S12425; S12426; S12427; S12429; S12432
R/Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A/Title: The smaller human V(H) gene families display remarkably little polymorphism.
A/Reference number: S09421; MUID:90059975; PMID:2511001
A/Accession: S12424
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-101 <SAS>
A/Cross-references: UNIPARC:UPI000011636C; EMBL:X56372
A/Superfamily: clones 5AU; 5BLK; 5CH; 5CW; 5LB; 5TT
A/Accession: S12425
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-101 <SA2>
A/Cross-references: UNIPARC:UPI000011636C; EMBL:X56373
A/Accession: S12426
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-101 <SA3>
A/Cross-references: UNIPARC:UPI000011636C; EMBL:X56370
A/Accession: S12427
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-101 <SA5>
A/Cross-references: UNIPARC:UPI000011636C; EMBL:X56369
A/Accession: S12432
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-101 <SA6>
A/Cross-references: UNIPARC:UPI000011636C; EMBL:X56371
C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin
F;18-101/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 101;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYPGDSDTTRYSPSFQ 17
|||||
Db 53 IYPGDSDTTRYSPSFQ 69

RESULT 5

PH1266
Ig heavy chain V region (clone VERG5) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C/Accession: PH1266
R/Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A/Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A/Reference number: PH1232; MUID:93018822; PMID:1402653
A/Accession: PH1266
A/Molecule type: mRNA
A/Residues: 1-102 <CAI>
A/Cross-references: UNIPARC:UPI0000176BD2
A/Superfamily: EBV-transformed CD5+ B cell [from adult PBL]
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYPGDSDTTRYSPSFQ 17
|||||
Db 54 IYPGDSDTTRYSPSFQ 70

RESULT 6

PH1279
Ig heavy chain V region (clones CLL11, CORD3, CORD4, CORD8, CORD9, CD+1, CD+3, CD+4, CD-
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C/Accession: PH1279
R/Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A/Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A/Reference number: PH1232; MUID:93018822; PMID:1402653
A/Accession: PH1279
A/Molecule type: DNA
A/Residues: 1-102 <CAI>
A/Cross-references: UNIPARC:UPI0000116D01
A/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Superfamily: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYPGDSDTTRYSPSFQ 17
|||||
Db 54 IYPGDSDTTRYSPSFQ 70

RESULT 7

PH1281
Ig heavy chain V region (clone PBL12) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PH1281
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chrom
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1281

A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Cross-references: UNIPARC:UPI0000176C67
A;Experimental source: adult PBL
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIVPGDSDTIYSPSFQ 17
Db 54 IIVPGDSDTYSPSFQ 70

RESULT 8

PH1277
Ig heavy chain V region (clone PBL8) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1277
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chrom
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1277
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Cross-references: UNIPARC:UPI0000176B41
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIVPGDSDTIYSPSFQ 17
Db 54 IIVPGDSDTYSPSFQ 70

RESULT 9

PH1244
Ig heavy chain V region (clone CORD2) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1244
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chrom
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1244
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Cross-references: UNIPARC:UPI0000176BC8
A;Experimental source: cord blood B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIVPGDSDTIYSPSFQ 17
Db 54 IIVPGDSDTYSPSFQ 70

RESULT 10

PH1267
Ig heavy chain V region (clone VERG9) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1267
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chrom
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1267
A;Molecule type: mRNA
A;Residues: 1-102 <CAI>
A;Cross-references: UNIPARC:UPI0000176BD3
A;Experimental source: EBV-transformed CD5+ B cell [from adult PBL]
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIVPGDSDTIYSPSFQ 17
Db 54 IIVPGDSDTYSPSFQ 70

RESULT 11

PH1272
Ig heavy chain V region (clone PBL3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1272
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chrom
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1272
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Cross-references: UNIPARC:UPI0000176C6C
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIVPGDSDTIYSPSFQ 17
Db 54 IIVPGDSDTYSPSFQ 70

RESULT 12

PH1282
Ig heavy chain V region (clone PBL13) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1282
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chrom
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1282

A:Molecule type: DNA
A:Residues: 1-102 <CAI>
A:Cross-references: UNIPARC:UPI0000176C68
A:Experimental source: adult PBL
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYFGDSDTIYSPSFQ 17
| | | | | | | | | | | | | | | | | |
Db 54 IYFGDSDTIYSPSFQ 70

RESULT 13

PH1248
Ig heavy chain V region (clone CORD6) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1248
R;Cal, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A:Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron

A:Reference number: PH1232; MUID:93018822; PMID:1402653
A:Accession: PH1248
A:Molecule type: DNA
A:Residues: 1-102 <CAI>
A:Cross-references: UNIPARC:UPI0000176A4E
A:Experimental source: cord blood B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYFGDSDTIYSPSFQ 17
| | | | | | | | | | | | | | | | | |
Db 54 IYFGDSDTIYSPSFQ 70

RESULT 14

PH1280
Ig heavy chain V region (clone PBL11) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1280
R;Cal, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A:Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron

A:Reference number: PH1232; MUID:93018822; PMID:1402653
A:Accession: PH1280
A:Molecule type: DNA
A:Residues: 1-102 <CAI>
A:Cross-references: UNIPARC:UPI0000176B42
A:Experimental source: adult PBL
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYFGDSDTIYSPSFQ 17
| | | | | | | | | | | | | | | | | |
Db 54 IYFGDSDTIYSPSFQ 70

RESULT 15

PH1258
Ig heavy chain V region (clone CD-2) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1258
R;Cal, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A:Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron

A:Reference number: PH1232; MUID:93018822; PMID:1402653
A:Accession: PH1258
A:Molecule type: DNA
A:Residues: 1-102 <CAI>
A:Cross-references: UNIPARC:UPI0000176BCD
A:Experimental source: cord blood B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYFGDSDTIYSPSFQ 17
| | | | | | | | | | | | | | | | | |
Db 54 IYFGDSDTIYSPSFQ 70

Search completed: December 3, 2005, 14:33:34
Job time : 4.64898 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 14:11:48 ; Search time 29.9755 Seconds
(without alignments)
400.126 Million cell updates/sec

Title: US-10-769-144-14
Perfect score: 92
Sequence: 1 ILYPGDSITYSPSQFQ 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	65.2	474	2	Q8R3H6 mouse
2	59	64.1	118	2	Q921C4 mouse
3	57	62.0	111	2	Q9D9B8 mouse
4	56	60.9	483	2	Q52L53 mouse
5	56	60.9	614	2	Q7TMT6 mouse
6	54	58.7	110	2	Q9JL83 mouse
7	54	58.7	120	2	Q5F2I1 mouse
8	53	57.6	481	2	Q91WT1 mouse
9	52	56.5	117	1	HV52 mouse
10	52	56.5	463	2	Q99LC4 mouse
11	51	55.4	117	1	HV06 mouse
12	51	55.4	909	2	Q6WJ05 GOSHI
13	49	53.3	193	2	Q4H3H2 CIOIN
14	49	53.3	590	2	Q4V9V8 mouse
15	49	53.3	860	2	Q4RR84 TETNG
16	48	52.2	573	2	Q6AHL9 LEIXX
17	48	52.2	958	2	Q415Z0 GIBZE
18	48	52.2	1216	1	AEGP RAT
19	47	51.1	330	2	Q93KW0 STRVR
20	47	51.1	458	2	Q5B7Z2 RAT
21	47	51.1	464	2	Q6FP95 mouse
22	47	51.1	555	2	Q5A204 CANAL
23	47	51.1	558	2	Q5A255 CANAL
24	47	51.1	567	2	Q26602 METHH
25	46	50.0	117	1	HV05 mouse
26	46	50.0	513	2	Q5UQP4 MIMIV
27	46	50.0	519	2	Q5EBM2 HUMAN
28	46	50.0	537	2	Q6GNX4 XENLA
29	45	48.9	198	2	Q5ARM8 EMENI
30	45	48.9	513	2	Q52572 PSESP
31	45	48.9	529	2	Q414V2 GIBZE

RESULT 1									
Q8R3H6_MOUSE									
ID	Q8R3H6_MOUSE	PRELIMINARY;							
AC	Q8R3H6_								
DT	01-JUN-2002	(Tremblrel. 21, Created)							
DT	01-JUN-2002	(Tremblrel. 21, Last sequence update)							
DT	01-MAR-2004	(Tremblrel. 26, Last annotation update)							
DE	IgH protein.								
GN	Name=IgH; Synonyms=AU044919;								
OS	Mus musculus (Mouse).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;								
OC	Muridea; Muridae; Murinae; Mus.								
OX	NCBI_TaxID=10090;								
EN	[1]								
RP	NUCLEOTIDE SEQUENCE.								
RC	STRAIN=CZBECH II;								
RC	TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;								
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;								
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,								
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,								
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,								
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,								
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,								
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,								
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,								
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,								
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,								
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,								
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,								
RA	Pahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,								
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,								
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,								
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,								
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,								
RT	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;								
RT	"Generation and initial analysis of more than 15,000 full-length human								
RT	and mouse cDNA sequences."								
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).								
RL	[2]								
RP	NUCLEOTIDE SEQUENCE.								
RC	STRAIN=CZBECH II;								
RC	TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;								
RA	Director MGC Project;								
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.								
DR	EMBL; BC025447; AAH25447.1; -, mRNA.								
DR	HSSP; P01869; 1CL7.								
DR	SMR; Q8R3H6; 20-470.								
DR	MGI; MGI:2144967; AU044919.								
DR	MGI; MGI:2144967; IgH.								
DR	GO; GO:0003823; F:ancigen binding; IEA.								
DR	InterPro; IPR007110; Ig-like.								
DR	InterPro; IPR003597; Ig cl.								
DR	InterPro; IPR003006; Ig_MHC.								

Q4n689 theileria P
Q9x224 drosophila
Q54nu3 dictyosteli
P98157 gallus gall
Q925e3 mus musculus
Q6fsy3 candida gla
P15110 burkholderi
Q41v17 burkholderi
Q9rvn0 deinococcus
Q61rd1 caenorhabdi
P0a058 staphylococ
P21867 escherichia
Q7uxi2 rhodospirall
Q9a5b6 caulobacter

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DR InterPro: IPR003596; IG.v.
DR Pfam: PF07654; CI-set; 3.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 4.
DR PROSITE: PS00290; IG MHC; UNKNOWN_1.
KW Immunoglobulin domain.
SQ SEQUENCE 474 AA; 51749 MW; 8608B576CD2874A CRC64;

Query Match 65.2%; Score 60; DB 2; Length 474;
Best Local Similarity 68.8%; Pred. NO. 0.59;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 2 IYPGDSPTIYSPFSQ 17
Db 70 IFPGDGDTHYSGKFG 85

RESULT 2
ID Q9Z1C4_MOUSE PRELIMINARY; PRT; 118 AA.
AC Q9Z1C4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-porcine VCAM mAb 3F4 heavy chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/C;
RX MEDLINE=97450619; PubMed=9307060; DOI=10.1016/S0161-5890(97)00042-4;
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT endothelial cells.";
RL Mol. Immunol. 34:441-452(1997).
DR EMBL: U78801; AAD00293.1; -; mRNA.
DR HSSP: P01751; INQB.
DR SMR: Q9Z1C4; 1-118.
DR Ensembl: ENSMUSG00000021155; Mus musculus.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG.v.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 13036 MW; 90BEC559D31EC4FC CRC64;

Query Match 64.1%; Score 59; DB 2; Length 118;
Best Local Similarity 62.5%; Pred. NO. 0.17;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 2 IYPGDSPTIYSPFSQ 17
Db 51 IYPGDSPTIYTKFERG 66

RESULT 3
ID Q9D9B8_MOUSE PRELIMINARY; PRT; 111 AA.
AC Q9D9B8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:170011011 product:immunoglobulin heavy chain 6 (heavy
DE chain of IgM), full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

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RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Nomura R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK007163; BAB24877.1; -, mRNA.
DR HSSP; P01820; 1G7J.
DR SMR; Q9D988; 7-106.
DR Ensembl; ENSMUSG00000063520; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS003596; IGV.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 111 AA; 11976 MW; 874DDF7BD98BD7B2 CRC64;

Query Match 62.0%; Score 57; DB 2; Length 111;
Best Local Similarity 62.5%; Pred. No. 0.34;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IYPGDSPTIYSPSPQ 17
| | | | | : | : |
Db 57 IYPGDGTNYGKFKG 72

RESULT 4
Q52L51_MOUSE PRELIMINARY; PRT; 483 AA.
AC Q52L51;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.H.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RG NIH WGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC094065; AAH94065.1; -, mRNA.
DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 483 AA; 52167 MW; CQFDB9168795FEB4 CRC64;

Query Match 60.9%; Score 56; DB 2; Length 483;
Best Local Similarity 62.5%; Pred. No. 2.7;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IYPGDSPTIYSPSPQ 17
| | | | | : | : |
Db 70 IYPGDGTNYGKFKG 85

RESULT 5
Q7TMT6_MOUSE PRELIMINARY; PRT; 614 AA.
AC Q7TMT6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC60843 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053409; AAH53409.1; -, mRNA.
DR HSSP; P01820; 1G7J.
DR Ensembl; ENSMUSG00000054328; Mus musculus.
DR GO; GO:0003823; F-antigen binding; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 4.

```

DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 5.
DR PROSITE; PS00290; IG MHC; UNKNOWN_3.
KW Immunoglobulin domain.
SQ SEQUENCE 614 AA; 67747 MW; 839BAF3BBD124F89 CRC64;
Query Match 60.9%; Score 56; DB 2; Length 614;
Best Local Similarity 56.2%; Pred. No. 3.5;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 2 IYPGDSDTIYSPSQG 17
Db 70 IYPGDDTNYNGKPKG 85

RESULT 6
Q9JL83 MOUSE
ID Q9JL83 MOUSE PRELIMINARY; PRT; 110 AA.
AC Q9JL83
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=BALB/c;
RX MEDLINE=20448942; PubMed=10992488;
RX DOI=10.1128/IAI.68.10.5803-5808.2000;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin."
RL Infect. Immun. 68:5803-5808 (2000).
RL EMBL; AF206023; AAF69321.1; -; mRNA.
DR HSSP; P01751; INQB.
DR SMR; Q9JL83; 1-110.
DR Ensembl; ENSMUSG00000063520; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 110
SQ SEQUENCE 110 AA; 12052 MW; 84E6F2AD219AF95E CRC64;
Query Match 58.7%; Score 54; DB 2; Length 110;
Best Local Similarity 56.2%; Pred. No. 1;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy 2 IYPGDSDTIYSPSQG 17
Db 43 IYPGDDAYNGKPKG 58

RESULT 7
Q5F2I1 MOUSE
ID Q5F2I1 MOUSE PRELIMINARY; PRT; 120 AA.
AC Q5F2I1
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Gamma heavy chain variable region (Fragment).
GN Name=IgG1 anti-TS1 VH;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN 1
RP NUCLEOTIDE SEQUENCE.
RA Erlendsson A.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ884574; CAI56336.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 120
SQ SEQUENCE 120 AA; 13087 MW; 4A6013141AB87BE2 CRC64;
Query Match 58.7%; Score 54; DB 2; Length 120;
Best Local Similarity 56.2%; Pred. No. 1.1;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 2 IYPGDSDTIYSPSQG 17
Db 51 IYPGNGDTYNGKPKG 66

RESULT 8
Q91WT1 MOUSE
ID Q91WT1 MOUSE PRELIMINARY; PRT; 481 AA.
AC Q91WT1
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN 1
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;

```

RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013490; AAH13490.1; -, mRNA.
DR HSSP; P01751; 1AGW.

DR Ensembl; ENSMUSG0000021155; Mus musculus.
DR GO; GO:0003823; P:antigen binding; IEA.

DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.

DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.

DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.

KW Immunoglobulin domain.
SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Query Match 57.6%; Score 53; DB 2; Length 481;
Best Local Similarity 56.2%; Pred. No. 8.2;

Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Oy 2 IYPGSDTRIYSPSQG 17
Db 70 IYPGDKTYNEKFKG 85

||||| :|:|:|
| | | | |

RESULT 9

HV52 MOUSE STANDARD; PRT; 117 AA.
ID HV52 MOUSE PRT; 117 AA.

AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Ig heavy chain V region VH58 A1/A4 precursor.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RN [1]
RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=85099340; PubMed=2578321; DOI=10.1016/0092-8674(85)90141-2;
RA Yancopoulos G.D., Alt F.W.;

RT "Developmentally controlled and tissue-specific expression of
unrearranged VH gene segments.";

RL Cell 40:271-281(1985).
CC This Swiss-Prot entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC -----
CC EMBL; M13787; AAA38499.1; -, mRNA.
CC PIR; A02029; HVMSA1.

DR HSSP; P01820; 1G7J.
DR SMR; P06327; 20-117.

DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.

DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.

KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19

FT CHAIN 20 117 Ig heavy chain V region VH58 A1/A4.
FT REGION 20 49 Framework-1.

FT REGION 50 54 Complementarity-determining-1.
FT REGION 55 68 Framework-2.

FT REGION 69 85 Complementarity-determining-2.
FT REGION 86 117 Framework-3.

FT DISULFID 41 115 By similarity.
FT NON_TER 117 117

SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;
Query Match 56.5%; Score 52; DB 1; Length 117;

Best Local Similarity 56.2%; Pred. No. 2.3;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Oy 2 IYPGSDTRIYSPSQG 17
Db 70 IYPGDKTYNEKFKG 85

||||| :|:|:|
| | | | |

RESULT 10

O99LC4 MOUSE PRELIMINARY; PRT; 463 AA.
ID O99LC4 MOUSE PRELIMINARY; PRT; 463 AA.

AC O99LC4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Igh-4 protein.
GN Name=Igh-4;

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N;

RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC virgin mouse. Taken by biopsy.;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Faney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N;

RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC virgin mouse. Taken by biopsy.;

RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC003435; AAH03435.1; -, mRNA.
DR PIR; B45837; B45837.

DR HSSP; P01869; 1CLU7.
DR SMR; O99LC4; 21-459.

DR MGI; MGI:96446; Igh-4.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.

DR GO; GO:0003823; P:antigen binding; IDA.
DR GO; GO:0001973; P:antibacterial humoral response (sensu Verte...; IDA.

DR GO; GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.
DR GO; GO:0006958; P:complement activation, classical pathway; IDA.

DR GO; GO:0042830; P:defense response to pathogenic bacteria; IDA.
DR GO; GO:0006911; P:phagocytosis, engulfment; IDA.

DR GO; GO:0006910; P:phagocytosis, recognition; IDA.
DR GO; GO:0005078; P:positive regulation of immune response; IDA.

DR GO; GO:0005076; P:positive regulation of type I hypersensitivity; IDA.
DR GO; GO:0001812; P:positive regulation of type I hypersensitivity; IDA.

DR GO; GO:0001798; P:positive regulation of type IIA hypersensit...; IDA.
DR InterPro; IPR007110; Ig-like.

```
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
KW Immunoglobulin domain.
SQ SEQUENCE 463 AA; 51008 MW; EAA674C6BBC30783 CRC64;

Query Match 56.5%; Score 52; DB 2; Length 463;
Best Local Similarity 56.2%; Pred. No. 11;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 IYPGSDSTIYSPSFOG 17
|||||:|||||:|:|
Db 70 IYPGSGNTIYSEKPKG 85

RESULT 11
ID HV06 MOUSE STANDARD; PRT; 117 AA.
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region 102 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RX MBLDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
RA Bothwell A.L.M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: This germline gene belongs to a set of closely
CC related genes that could encode V regions of Npb antibodies.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A02032; HVMS02.
DR PDB; 1QNZ; NMR; H=21-117.
DR Ensembl; ENSMUSG0000062849; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW 3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 Ig heavy chain V region 102.
FT REGION 20 49 Framework-1.
FT REGION 50 54 Complementarity-determining-1.
FT REGION 55 68 Framework-2.
FT REGION 69 85 Complementarity-determining-2.
FT REGION 86 117 Framework-3.
FT DISULFID 41 115 By similarity.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FCA8C CRC64;

Query Match 55.4%; Score 51; DB 1; Length 117;
Best Local Similarity 56.2%; Pred. No. 3.4;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IYPGSDSTIYSPSFOG 17
|:|:|||||:|:|
Db 70 IYPGSGNTIYSEKPKG 85
```

```
Db 70 IHPSDSDTNYNQKPKG 85

RESULT 12
Q6WJ05 GOSHI
ID Q6WJ05 GOSHI PRELIMINARY; PRT; 909 AA.
AC Q6WJ05;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Central motor kinesin 1.
OS Name=CWKL;
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lu L., Lee Y.-R.J., Pan R., Liu B.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY283056; AAQ18797.1; -; mRNA.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005575; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
DR PROSITE; PS00667; KINESIN MOTOR DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
SQ SEQUENCE 909 AA; 100815 MW; 424E3C6DF67EDF4F CRC64;

Query Match 55.4%; Score 51; DB 2; Length 909;
Best Local Similarity 64.3%; Pred. No. 36;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 PGDSDTIYSPSFOG 17
|||||:|||||:|:|
Db 115 PGTSDFYSPFPRG 128

RESULT 13
Q4H3H2 CIOIN
ID Q4H3H2 CIOIN PRELIMINARY; PRT; 193 AA.
AC Q4H3H2;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Fringe (Fragment).
GN Name=Ci-Fringe 4;
OS Ciona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Cionidae; Ciona.
OX NCBI_TaxID=7719;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15269171; DOI=10.1242/dev.01270;
RA Imai K.S., Hino K., Yagi K., Satoh N., Satou Y.;
RT "Genomewide surveys of developmentally relevant genes in Ciona
RT intestinalis."
RL Development 131:4047-4058(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE
RX PubMed=12736827; DOI=10.1007/s00427-003-0330-z;
RA Satou Y., Satoh N.;
RT "Genomewide surveys of developmentally relevant genes in Ciona
RT intestinalis."
RL Dev. Genes Evol. 213:211-212(2003).
RN [3]
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RP NUCLEOTIDE SEQUENCE.
RT "Expressed genes in Ciona intestinalis.";
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB210450; BAE06455.1; -, mRNA.
FT NON_TER 1
SQ SEQUENCE 193 AA; 22222 MW; B93C2D76BD07D6C2 CRC64;

Query Match 53.3%; Score 49; DB 2; Length 193;
Best Local Similarity 52.9%; Pred. No. 13;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Oy 1 IYPGSDSDTIYSPSQFQ 17
Db 27 LIYPGSSDVTYPIGKG 43

RESULT 14
Q4V9V8 MOUSE PRELIMINARY; PRT; 590 AA.
AC Q4V9V8
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN Name=Igh-6;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H.K., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguercio N.J., Peters G.J., Abramson R.D., Mullahy S.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Smallos D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
RG NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC096667; AAH96667.1; -, mRNA.
DR MGI; MGI:96446; Igh-6.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.

KW Hypothetical protein.
SQ SEQUENCE 590 AA; 64892 MW; D425318F9A188B14 CRC64;

Query Match 53.3%; Score 49; DB 2; Length 590;
Best Local Similarity 50.0%; Pred. No. 46;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Oy 2 IYPGSDSDTIYSPSQFQ 17
Db 70 IYPGSGNTYNEKFKG 85

RESULT 15
Q4RR84 TETNG PRELIMINARY; PRT; 860 AA.
AC Q4RR84
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 14 SCAF15003, whole genome shotgun sequence.
(Fragment).
GN ORFNames=GSTENG0030281001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallou O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anhouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957 (2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; CAAB01015003; CAG09098.1; -, Genomic_DNA.
DR NON_TER 1
SQ SEQUENCE 860 AA; 95101 MW; 5868355B6346C75 CRC64;

Query Match 53.3%; Score 49; DB 2; Length 860;
Best Local Similarity 61.5%; Pred. No. 71;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 2 IYPGSDSDTIYSPS 14
Db 278 LHPGDFDIVQSPS 290

Search completed: December 3, 2005, 14:32:24
Job time : 30.9755 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 13:24:58 ; Search time 7.21633 Seconds
(without alignments)
194.765 Million cell updates/sec

Title: US-10-769-144-14
Perfect score: 92
Sequence: 1 IIPQDSPTIYSPFQG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	92.4	98	1	US-08-478-039-81
2	85	92.4	98	1	US-08-476-349A-81
3	85	92.4	98	1	US-08-665-202-33
4	85	92.4	98	2	US-09-315-574-33
5	85	92.4	98	2	US-10-194-975-45
6	85	92.4	111	2	US-09-726-219A-171
7	85	92.4	111	2	US-09-196-522-171
8	85	92.4	117	2	US-08-545-809A-133
9	85	92.4	117	2	US-09-515-697-133
10	85	92.4	119	2	US-09-025-769B-26
11	85	92.4	119	2	US-09-490-070A-26
12	85	92.4	119	2	US-09-490-153-26
13	85	92.4	119	2	US-09-490-324-26
14	85	92.4	120	2	US-09-025-769B-40
15	85	92.4	120	2	US-09-025-769B-67
16	85	92.4	120	2	US-09-490-070A-40
17	85	92.4	120	2	US-09-490-070A-67
18	85	92.4	120	2	US-09-490-153-40
19	85	92.4	120	2	US-09-490-153-67
20	85	92.4	120	2	US-09-490-324-40
21	85	92.4	120	2	US-09-490-324-67
22	84	91.3	125	1	US-08-665-202-56
23	84	91.3	125	2	US-09-315-574-56
24	83	90.2	125	1	US-08-665-202-44
25	83	90.2	125	1	US-08-665-202-45
26	83	90.2	125	1	US-08-665-202-46
27	83	90.2	125	1	US-08-665-202-47

28	83	90.2	125	1	US-08-665-202-48	Sequence 48, Appl
29	83	90.2	125	1	US-08-665-202-49	Sequence 49, Appl
30	83	90.2	125	1	US-08-665-202-50	Sequence 50, Appl
31	83	90.2	125	1	US-08-665-202-51	Sequence 51, Appl
32	83	90.2	125	1	US-08-665-202-52	Sequence 52, Appl
33	83	90.2	125	1	US-08-665-202-53	Sequence 53, Appl
34	83	90.2	125	1	US-08-665-202-54	Sequence 54, Appl
35	83	90.2	125	1	US-08-665-202-55	Sequence 55, Appl
36	83	90.2	125	1	US-08-665-202-57	Sequence 57, Appl
37	83	90.2	125	1	US-08-665-202-58	Sequence 58, Appl
38	83	90.2	125	2	US-09-315-574-44	Sequence 44, Appl
39	83	90.2	125	2	US-09-315-574-45	Sequence 45, Appl
40	83	90.2	125	2	US-09-315-574-46	Sequence 46, Appl
41	83	90.2	125	2	US-09-315-574-47	Sequence 47, Appl
42	83	90.2	125	2	US-09-315-574-48	Sequence 48, Appl
43	83	90.2	125	2	US-09-315-574-49	Sequence 49, Appl
44	83	90.2	125	2	US-09-315-574-50	Sequence 50, Appl
45	83	90.2	125	2	US-09-315-574-51	Sequence 51, Appl

RESULT 1
US-08-478-039-81
; Sequence 81, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SNECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant

ALIGNMENTS

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/ TOPOLOGY: not relevant
/ MOLECULE TYPE: peptide
/ ORIGINAL SOURCE:
/ ORGANISM: Homo sapiens
/ POSITION IN GENOME:
/ CHROMOSOME/SEGMENT: VH5 consensus
US-08-478-039-81

Query Match          92.4%; Score 85; DB 1; Length 98;
Best Local Similarity 94.1%; Pred. No. 2.7e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTIYSPSFQ 17
Db 50 IIYPGDSDTIYSPSFQ 66

RESULT 2
US-08-476-349A-81
; Sequence 81, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476.349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VH5 consensus

US-08-476-349A-81
Query Match          92.4%; Score 85; DB 1; Length 98;
Best Local Similarity 94.1%; Pred. No. 2.7e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTIYSPSFQ 17
Db 50 IIYPGDSDTIYSPSFQ 66

RESULT 3
US-08-665-202-33
; Sequence 33, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; MOLECULE TYPE: peptide
US-08-665-202-33

Query Match          92.4%; Score 85; DB 1; Length 98;
Best Local Similarity 94.1%; Pred. No. 2.7e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTIYSPSFQ 17
Db 50 IIYPGDSDTIYSPSFQ 66

RESULT 4
US-09-315-574-33
; Sequence 33, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
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APPLICANT: Marks, James D.
 APPLICANT: Schier, Robert
 TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
 Tumor Antigens
 TITLE OF INVENTION: Tumor Antigens
 NUMBER OF SEQUENCES: 141
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.
 STREET: Four Embarcadero Center, Suite 1100
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-4106
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/315,574
 FILING DATE: 20-MAY-99
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/000,238
 FILING DATE: 14-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/000,250
 FILING DATE: 15-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/665,202
 FILING DATE: 13-JUN-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Hunter, Tom
 REGISTRATION NUMBER: 38,498
 REFERENCE/DOCKET NUMBER: 02307E-061411
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 33:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 98 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-315-574-33

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Query Match      92.4%; Score 85; DB 2; Length 98;
Best Local Similarity 94.1%; Pred. No. 2.7e-05;
Matches 16: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 IYPGDSDTIYSPSQG 17
 |||||
p6 50 IYPGDSDTRYSPSQG 66

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RESULT 5
US-10-134-975-45
; Sequence 45, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-10-194-975-45

Query Match          92.4%; Score 85; DB 2; Length 98;
Best Local Similarity 94.1%;
Matches 16; Conservative 0; Mismatches 1; Indels

Qy  1 IYPGDSDTIYSPFQ 17
      |||||
Db  50 IYPGDSDTIYSPFQ 66

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RESULT 6
US-09-726-219A-171
; Sequence 171, Application US/09726219A
; Patent No. 6806079
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clarkson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing
; FILE REFERENCE: 213839-00013
; CURRENT APPLICATION NUMBER: US/09726,219A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 171
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-726-219A-171

```

Query Match	92.4%;	Score 85;	DB 2;	Length 111;
Best Local Similarity	94.1%;	Pred. No. 3.1e-05;		
Matches 16;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	IIYPGDSDTIYSPSFQG	17	
Dd	50	IIYPGDSDTIYSPSFQG	66	

RESULT 7
US-09-196-522-171
; Sequence 171, Application US/09196522

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US-10-194-975-45

Query Match      92.4%; Score 85; DB 2; Length 98;
Best Local Similarity 94.1%; Pred. No. 2.7e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 IYPGSDTIIYSPSQG 17
        |||||
Db       50 IYPGSDTRYSPSQG 66
        |||||

RESULT 6
US-09-726-219A-171
; Sequence 171, Application US/09726219A
; Patent No. 6806079
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 213839-00013
; CURRENT APPLICATION NUMBER: US/09/726,219A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 171
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-726-219A-171

Query Match      92.4%; Score 85; DB 2; Length 111;
Best Local Similarity 94.1%; Pred. No. 3.1e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 IYPGSDTIIYSPSQG 17
        |||||
Db       50 IYPGSDTRYSPSQG 66
        |||||

RESULT 7
US-09-196-522-171
; Sequence 171, Application US/09196522

```

Patent No. 6916605
GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
APPLICANT: Pope, Anthony
APPLICANT: Johnson, Kevin
APPLICANT: Hoogenboom, Hendricus
APPLICANT: Griffiths, Andrew
APPLICANT: Jackson, Ronald
APPLICANT: Holliger, Kasper
APPLICANT: Marks, James
APPLICANT: Clarkson, Timothy
APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Bonert, Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 213839-00004
CURRENT APPLICATION NUMBER: US/09/196,522
CURRENT FILING DATE: 1998-11-28
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9024503.6
PRIOR FILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR FILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR FILING DATE: 1993-01-08
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: Patent in version 3.1
SEQ ID NO 171
LENGTH: 111
TYPE: PRT
ORGANISM: Homo sapiens
US-09-196-522-171

Query Match 92.4%; Score 85; DB 2; Length 111;
Best Local Similarity 94.1%; Pred. No. 3.1e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIYPGSDTIYSPSQ 17
Db 50 IIYPGSDTIYSPSQ 66

RESULT 8
US-08-545-809A-133
Sequence 133, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804

Query Match 92.4%; Score 85; DB 2; Length 111;
Best Local Similarity 94.1%; Pred. No. 3.1e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIYPGSDTIYSPSQ 17
Db 50 IIYPGSDTIYSPSQ 66

RESULT 8
US-08-545-809A-133
Sequence 133, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-545-809A-133

Query Match 92.4%; Score 85; DB 2; Length 117;
Best Local Similarity 94.1%; Pred. No. 3.3e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIYPGSDTIYSPSQ 17
Db 69 IIYPGSDTIYSPSQ 85

RESULT 9
US-09-515-697-133
Sequence 133, Application US/09515697
Patent No. 6936705
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/515,697
FILING DATE: 29-Feb-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809
FILING DATE: 27-MAR-1996
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906

TELEX: 200154
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 133:
US-09-515-697-133

Query Match 92.4%; Score 85; DB 2; Length 117;
Best Local Similarity 94.1%; Pred. No. 3.3e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYFGSDTIYSPSQG 17
Db 69 IYFGSDTIYSPSQG 85

RESULT 10
US-09-025-769B-26
; Sequence 26, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-025-769B-26

Query Match 92.4%; Score 85; DB 2; Length 119;
Best Local Similarity 94.1%; Pred. No. 3.3e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYFGSDTIYSPSQG 17
Db 50 IYFGSDTIYSPSQG 66

RESULT 11
US-09-490-070A-26
; Sequence 26, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Colin G. Sandercock, Esq.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 912-2000

TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 26:

US-09-490-070A-26

Query Match 92.4%; Score 85; DB 2; Length 119;
Best Local Similarity 94.1%; Pred. No. 3.3e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYFGSDTIYSPSQG 17
Db 50 IYFGSDTIYSPSQG 66

RESULT 12
US-09-490-153-26
; Sequence 26, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;; STREET: 1251 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10021
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; FILING DATE: 24-Jan-2000
;; PRIORITY APPLICATION NUMBER: US/09/490,153
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/025,769B
;; FILING DATE: 18-FEB-1998
;; APPLICATION NUMBER: EP 95 11 3021.0
;; FILING DATE: 18-AUG-1995
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: James F. Haley, Jr., Esq.
;; REGISTRATION NUMBER: 27,794
;; REFERENCE/DOCKET NUMBER: MORPHO/5
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)596-9000
;; TELEFAX: (212)596-9090
;;
;; INFORMATION FOR SEQ ID NO: 26:
;; SEQUENCE CHARACTERISTICS:
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-153-26

Query Match 92.4%; Score 85; DB 2; Length 119;
Best Local Similarity 94.1%; Pred. No. 3.3e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYFGSDTIYSPSQ 17
Db 50 IYFGSDTIYSPSQ 66

RESULT 13
US-09-490-324-26
; Sequence 26, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324

;; FILING DATE: 24-Jan-2000
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/025,769
;; FILING DATE: 18-FEB-1998
;; APPLICATION NUMBER: EP 95 11 3021.0
;; FILING DATE: 18-AUG-1995
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: James F. Haley, Jr., Esq.
;; REGISTRATION NUMBER: 27,794
;; REFERENCE/DOCKET NUMBER: MORPHO/5
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)596-9000
;; TELEFAX: (212)596-9090
;;
;; INFORMATION FOR SEQ ID NO: 26:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 119 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-324-26

Query Match 92.4%; Score 85; DB 2; Length 119;
Best Local Similarity 94.1%; Pred. No. 3.3e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYFGSDTIYSPSQ 17
Db 50 IYFGSDTIYSPSQ 66

RESULT 14
US-09-025-769B-40
; Sequence 40, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids

;
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-40

Query Match 92.4%; Score 85; DB 2; Length 120;
Best Local Similarity 94.1%; Pred. No. 3.4e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYPGSDTIYSPSQG 17
|||||
Db 50 IYPGSDTIYSPSQG 66

RESULT 15

US-09-025-769B-67
; Sequence 67, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION NUMBER: US/09/025,769B
; APPLICATION DATA:
; FILING DATE: 18-AUG-1995
; APPLICATION NUMBER: EP 95 11 3021.0
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-67

Query Match 92.4%; Score 85; DB 2; Length 120;
Best Local Similarity 94.1%; Pred. No. 3.4e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYPGSDTIYSPSQG 17
|||||
Db 50 IYPGSDTIYSPSQG 66

Search completed: December 3, 2005, 14:11:29
Job time : 7.21633 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 13:27:13 ; Search time 23.3143 Seconds
(without alignments)
304.667 Million cell updates/sec

Title: US-10-769-144-14

Perfect score: 92
Sequence: 1 IIYPGSDTIYSPSFQ 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA_Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	17	5	US-10-769-144-14
2	92	100.0	17	5	US-10-903-191-14
3	92	100.0	116	3	US-09-851-614-4
4	92	100.0	116	4	US-10-035-637-4
5	92	100.0	116	5	US-10-769-144-4
6	92	100.0	116	5	US-10-903-191-4
7	92	100.0	411	5	US-10-769-144-12
8	92	100.0	411	5	US-10-903-191-12
9	92	100.0	468	5	US-10-769-144-2
10	92	100.0	468	5	US-10-903-191-2
11	92	100.0	613	5	US-10-769-144-10
12	92	100.0	613	5	US-10-903-191-10
13	85	92.4	17	4	US-10-384-060-40
14	85	92.4	17	4	US-10-374-932-6
15	85	92.4	17	4	US-10-379-741-6
16	85	92.4	17	4	US-10-128-520-369
17	85	92.4	17	5	US-10-684-957-35
18	85	92.4	17	5	US-10-638-265-95
19	85	92.4	17	5	US-10-726-332-55
20	85	92.4	17	5	US-10-726-332-73
21	85	92.4	17	5	US-10-726-332-88
22	85	92.4	17	5	US-10-726-332-91
23	85	92.4	17	5	US-10-891-658-93
24	85	92.4	17	5	US-10-982-725-6
25	85	92.4	82	4	US-10-078-958-5
26	85	92.4	98	3	US-09-850-165-89
27	85	92.4	98	4	US-10-194-975-45

28	85	92.4	98	4	US-10-125-687-16
29	85	92.4	98	4	US-10-041-860-6
30	85	92.4	98	4	US-10-041-860-301
31	85	92.4	98	4	US-10-041-860-302
32	85	92.4	98	4	US-10-041-860-312
33	85	92.4	98	4	US-10-041-860-314
34	85	92.4	98	4	US-10-041-860-318
35	85	92.4	98	4	US-10-041-860-320
36	85	92.4	98	4	US-10-041-860-336
37	85	92.4	98	4	US-10-041-860-338
38	85	92.4	98	4	US-10-041-860-367
39	85	92.4	98	4	US-10-308-817-88
40	85	92.4	98	4	US-10-032-037B-106
41	85	92.4	98	4	US-10-032-037B-107
42	85	92.4	98	4	US-10-032-037B-108
43	85	92.4	98	4	US-10-029-988B-106
44	85	92.4	98	4	US-10-029-988B-107
45	85	92.4	98	4	US-10-029-988B-108

ALIGNMENTS

RESULT 1
US-10-769-144-14
; Sequence 14, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-14

Query Match 100.0%; Score 92; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIYPGSDTIYSPSFQ 17
| | | | | | | | | | | | | | | | | |
Db 1 IIYPGSDTIYSPSFQ 17

RESULT 2
US-10-903-191-14
; Sequence 14, Application US/10903191
; Publication No. US20050180983A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301CP
; CURRENT APPLICATION NUMBER: US/10/903,191
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/769144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979

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; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-903-191-14

Query Match      100.0%; Score 92; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIYPGSDTIYSPSQG 17
Db 1 IIYPGSDTIYSPSQG 17

RESULT 3
US-09-851-614-4
; Sequence 4, Application US/09851614
; Publication No. US20030167502A1
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Keler, Tibor
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
; FILE REFERENCE: MXI-166
; CURRENT APPLICATION NUMBER: US/09/851,614
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: USN 60/203,126
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: USN 60/230,739
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-851-614-4

Query Match      100.0%; Score 92; DB 3; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIYPGSDTIYSPSQG 17
Db 50 IIYPGSDTIYSPSQG 66

RESULT 4
US-10-035-637-4
; Sequence 4, Application US/10035637
; Publication No. US20030031667A1
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Keler, Tibor
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
; FILE REFERENCE: MXI-166CP
; CURRENT APPLICATION NUMBER: US/10/035,637
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 09/851,614
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USN 60/203,126
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: USN 60/230,739
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-035-637-4

Query Match      100.0%; Score 92; DB 4; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIYPGSDTIYSPSQG 17
Db 50 IIYPGSDTIYSPSQG 66

RESULT 5
US-10-769-144-4
; Sequence 4, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-4

Query Match      100.0%; Score 92; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIYPGSDTIYSPSQG 17
Db 50 IIYPGSDTIYSPSQG 66

RESULT 6
US-10-903-191-4
; Sequence 4, Application US/10903191
; Publication No. US20050180983A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; FILE REFERENCE: MXI-301CP
; CURRENT APPLICATION NUMBER: US/10/903,191
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/769144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-903-191-4

Query Match      100.0%; Score 92; DB 5; Length 116;
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Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IYPGDSDTIYSPSFQ 17
Db 50 IYPGDSDTIYSPSFQ 66

RESULT 7
US-10-769-144-12
; Sequence 12, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-12

Query Match 100.0%; Score 92; DB 5; Length 411;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IYPGDSDTIYSPSFQ 17
Db 191 IYPGDSDTIYSPSFQ 207

RESULT 8
US-10-903-191-12
; Sequence 12, Application US/10903191
; Publication No. US20050180983A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; FILE REFERENCE: MXI-301CP
; CURRENT APPLICATION NUMBER: US/10/903,191
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/769144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-903-191-12

Query Match 100.0%; Score 92; DB 5; Length 411;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IYPGDSDTIYSPSFQ 17
Db 50 IYPGDSDTIYSPSFQ 66

RESULT 7
US-10-769-144-12
; Sequence 12, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-12

Query Match 100.0%; Score 92; DB 5; Length 411;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IYPGDSDTIYSPSFQ 17
Db 191 IYPGDSDTIYSPSFQ 207

RESULT 8
US-10-903-191-12
; Sequence 12, Application US/10903191
; Publication No. US20050180983A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; FILE REFERENCE: MXI-301CP
; CURRENT APPLICATION NUMBER: US/10/903,191
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/769144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-903-191-12

Query Match 100.0%; Score 92; DB 5; Length 411;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IYPGDSDTIYSPSFQ 17
Db 50 IYPGDSDTIYSPSFQ 66

RESULT 7
US-10-769-144-12
; Sequence 12, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-2

Query Match 100.0%; Score 92; DB 5; Length 468;
Best Local Similarity 100.0%; Pred. No. 6.2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IYPGDSDTIYSPSFQ 17
Db 69 IYPGDSDTIYSPSFQ 85

RESULT 10
US-10-903-191-2
; Sequence 2, Application US/10903191
; Publication No. US20050180983A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; FILE REFERENCE: MXI-301CP
; CURRENT APPLICATION NUMBER: US/10/903,191
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/769144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-903-191-2

Query Match 100.0%; Score 92; DB 5; Length 468;
Best Local Similarity 100.0%; Pred. No. 6.2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IYPGDSDTIYSPSFQ 17
Db 69 IYPGDSDTIYSPSFQ 85

RESULT 11
US-10-769-144-10
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; Sequence 10, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-10

Query Match 100.0%; Score 92; DB 5; Length 613;
Best Local Similarity 100.0%; Pred. No. 8.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 IIYPGDSDTIYSPSQG 17
Db 69 IIYPGDSDTIYSPSQG 85

RESULT 12

US-10-903-191-10
; Sequence 10, Application US/10903191
; Publication No. US20050180983A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; FILE REFERENCE: MXI-301CP
; CURRENT APPLICATION NUMBER: US/10/903,191
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/769144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-903-191-10

Query Match 100.0%; Score 92; DB 5; Length 613;
Best Local Similarity 100.0%; Pred. No. 8.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 IIYPGDSDTIYSPSQG 17
Db 69 IIYPGDSDTIYSPSQG 85

RESULT 13

US-10-384-060-40
; Sequence 40, Application US/10384060
; Publication No. US20030226155A1
; GENERAL INFORMATION:
; APPLICANT: SADEGHI, Homayoun
; APPLICANT: PRIOR, Christopher P.

; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
; FILE REFERENCE: S4710-5004-US
; CURRENT APPLICATION NUMBER: US/10/384,060
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VH CDR2 sequence
US-10-384-060-40

Query Match 92.4%; Score 85; DB 4; Length 17;
Best Local Similarity 94.1%; Pred. No. 2e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 IIYPGDSDTIYSPSQG 17
Db 1 IIYPGDSDTIYSPSQG 17

RESULT 14

US-10-374-932-6
; Sequence 6, Application US/10374932
; Publication No. US20030235586A1
; GENERAL INFORMATION:
; APPLICANT: van de Winkel, Jan G.J.
; APPLICANT: van Dijk, Marcus Antonius
; APPLICANT: Schuurman, Janine
; APPLICANT: Gerritsen, Arnout F.
; APPLICANT: Baadsgaard, Ole
; APPLICANT: Petersen, Jorgen
; TITLE OF INVENTION: HUMAN ANTIBODIES SPECIFIC FOR INTERLEUKIN 15 (IL-15)
; FILE REFERENCE: GMI-024CP
; CURRENT APPLICATION NUMBER: US/10/374,932
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 60/314,731
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: US 10/226615
; PRIOR FILING DATE: 2002-08-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-374-932-6

Query Match 92.4%; Score 85; DB 4; Length 17;
Best Local Similarity 94.1%; Pred. No. 2e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 IIYPGDSDTIYSPSQG 17
Db 1 IIYPGDSDTIYSPSQG 17

RESULT 15

US-10-379-741-6
; Sequence 6, Application US/10379741
; Publication No. US20040071702A1
; GENERAL INFORMATION:

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; APPLICANT: van de Winkel, Jan G.J.
; APPLICANT: van Dijk, Marcus Antonius
; APPLICANT: Schuurman, Janine
; APPLICANT: Gerritsen, Arnout F.
; APPLICANT: Baadsgaard, Ole
; APPLICANT: Petersen, Jorgen
; TITLE OF INVENTION: HUMAN ANTIBODIES SPECIFIC FOR INTERLEUKIN 15 (IL-15)
; FILE REFERENCE: GMI-024CP2
; CURRENT APPLICATION NUMBER: US/10/379,741
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: US 60/314,731
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: US 10/226615
; PRIOR FILING DATE: 2002-08-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-379-741-6

Query Match      92.4%; Score 85; DB 4; Length 17;
Best Local Similarity 94.1%; Pred. No. 2e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 IIYPGDSDTIYSPSFQG 17
        |||||
Db      1 IIYPGDSDTIYSPSFQG 17
        |||||
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Search completed: December 3, 2005, 14:17:35
Job time : 24.3143 secs

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OM protein - protein search, using sw model

Run on: December 3, 2005, 13:48:29 ; Search time 0.971429 Seconds
(without alignments)
83.796 Million cell updates/sec

Title: US-10-769-144-14

Perfect score: 92

Sequence: 1 IYPGDSPTYSPSQ 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	85	92.4	98	7	US-11-054-669-45
2	85	92.4	98	7	US-11-084-554-56
3	85	92.4	252	7	US-11-054-515-1537
4	81	86.0	248	7	US-11-054-515-1995
5	80	87.0	249	7	US-11-054-515-1312
6	77	83.7	248	7	US-11-054-515-1
7	69	75.0	249	7	US-11-054-515-1957
8	61	66.3	119	7	US-11-054-669-124
9	58	63.0	248	6	US-10-512-184-36
10	58	63.0	615	6	US-10-512-184-50
11	57	62.0	17	6	US-10-502-145-27
12	57	62.0	121	6	US-10-502-145-21
13	57	62.0	247	7	US-11-084-717-21
14	57	62.0	543	6	US-10-495-664-3
15	56	60.9	248	7	US-11-054-515-2088
16	55	59.8	251	7	US-11-054-515-1390
17	54	58.7	247	7	US-11-084-717-23
18	54	58.7	247	7	US-11-084-717-25
19	53	57.6	247	7	US-11-054-515-2103
20	51	55.4	249	7	US-11-054-515-1970
21	48	52.2	17	6	US-10-839-799-116
22	48	52.2	98	7	US-11-054-669-11
23	48	52.2	117	6	US-10-839-799-132
24	48	52.2	125	7	US-11-096-074-58
25	48	52.2	136	6	US-10-839-799-29

26	48	52.2	136	6	US-10-839-799-99
27	48	52.2	269	6	US-10-839-799-109
28	47	51.1	117	6	US-10-932-334-76
29	47	51.1	118	6	US-10-507-662-35
30	46	50.0	98	7	US-11-054-669-5
31	46	50.0	98	7	US-11-084-554-17
32	46	50.0	118	6	US-10-507-662-34
33	45	48.9	118	6	US-10-507-662-33
34	45	48.9	119	7	US-11-054-669-123
35	45	48.9	253	7	US-11-054-515-1895
36	45	48.9	253	7	US-11-054-515-2098
37	45	48.9	254	7	US-11-054-515-1001
38	45	48.9	254	7	US-11-054-515-1334
39	44	47.8	247	7	US-11-054-515-3240
40	44	47.8	250	7	US-11-054-515-1952
41	44	47.8	251	7	US-11-054-515-1084
42	44	47.8	253	7	US-11-054-515-1951
43	44	47.8	253	7	US-11-054-515-2101
44	44	47.8	472	6	US-10-485-517-153
45	43	46.7	119	6	US-10-477-950-2

ALIGNMENTS

RESULT 1

US-11-054-669-45
; Sequence 45, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-45

Query Match 92.4%; Score 85; DB 7; Length 98;
Best Local Similarity 94.1%; Pred. NO. 9.8e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYPGDSPTYSPSQ 17
Db 50 IYPGDSPTYSPSQ 66

RESULT 2

US-11-084-554-56
; Sequence 56, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24

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; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-56

Query Match          92.4%; Score 85; DB 7; Length 98;
Best Local Similarity 94.1%; Pred. No. 9.8e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IIYPGSDTIYSPFQ 17
   ||||| |||||
Db 50 IIYPGSDTRYSPFQ 66

RESULT 3
US-11-054-515-1537
; Sequence 1537, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1995
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1995

Query Match          88.0%; Score 81; DB 7; Length 248;
Best Local Similarity 88.2%; Pred. No. 1.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IIYPGSDTIYSPFQ 17
   ||||| |||||
Db 50 IIYPGSDTRYSPFQ 66

RESULT 5
US-11-054-515-1312
; Sequence 1312, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1312
; LENGTH: 249
; TYPE: PRT
US-11-054-515-1312

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; ORGANISM: Homo sapiens
US-11-054-515-1312

Query Match      87.0%; Score 80; DB 7; Length 249;
Best Local Similarity 88.2%; Pred. No. 1.7e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYPGSDSTIYSPSQFQ 17
    |||||:|||||
Db 50 IYPGSDSTIYSPSQFQ 66

RESULT 6
US-11-054-515-1
; Sequence 1, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18

; ORGANISM: Homo sapiens
US-11-054-515-1

Query Match      83.7%; Score 77; DB 7; Length 248;
Best Local Similarity 82.4%; Pred. No. 5.2e-06;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 IYPGSDSTIYSPSQFQ 17
    |||||:|||||
Db 50 IYPGSDSTIYSPSQFQ 66

RESULT 7
US-11-054-515-1957
; Sequence 1957, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18

; ORGANISM: Homo sapiens
US-11-054-515-1

Query Match      87.7%; Score 77; DB 7; Length 248;
Best Local Similarity 82.4%; Pred. No. 5.2e-06;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 IYPGSDSTIYSPSQFQ 17
    |||||:|||||
Db 50 IYPGSDSTIYSPSQFQ 66

RESULT 8
US-11-054-669-124
; Sequence 124, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 124
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-124

Query Match      66.3%; Score 61; DB 7; Length 119;
Best Local Similarity 68.8%; Pred. No. 0.00096;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IYPGSDSTIYSPSQFQ 17
    |||:|||||
Db 51 IYPRSGDTSYNPSFQ 66

RESULT 9
US-10-512-184-36
; Sequence 36, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"orderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
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/ FILE REFERENCE: 3581.01US01
/ CURRENT APPLICATION NUMBER: US/10/512,184
/ CURRENT FILING DATE: 2004-10-22
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 36
/ LENGTH: 248
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artifi
/ OTHER INFORMATION: specificity against S
/ OTHER INFORMATION: originates from Mus m
US-10-512-184-36

```

Query Match 63.0%; Score 58; DB 6; Length 248;
Best Local Similarity 62.5%; Pred. No. 0.0064;
Matches 10; Conservative 3; Mismatches 3; Indels

Qy 2 YPGDSDTIYSPSQG 17
|||:||||:|:
Db 53 YPGNSDTSYNQKFKG 68

RESULT 10
US-10-512-184-50
; Sequence 50, Application US/10512184
; Publication No. US2005024901A1
; GENERAL INFORMATION:

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Query Match          63.0%; Score 58; DB 6; Length 615;
Best Local Similarity 62.5%; Pred. No. 0.017;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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Qy 2 IYPGDSDTIYSPSQ 17
|||:||||:|:
Db 394 IYPCGSDTSYNQKFKG 409

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RESULT 11
US-10-502-145-27
Sequence 27, Application US/10502145
Publication No. US2005024406A1
GENERAL INFORMATION:
APPLICANT: MACKAY, CHARLES REAY
TITLE OF INVENTION: Anti-Csa antibodies
FILE REFERENCE: RICE-032
CURRENT APPLICATION NUMBER: US/10/502,145
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: USSN 60/350,961
PRIOR FILING DATE: 2002-01-25
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 17

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; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-502-145-27

Query Match 62.0%; Score 57; DB 6; Length 17;
Best Local Similarity 62.5%; Pred. NO. 0.00056;
Matches 10; Conservative 2; Mismatches 4; Indels

Qy 2 YPGDSDTIYSPSQ 17
||| | | : |
Db 2 YPGDGDTKYNGKFKG 17

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RESULT 12
US-10-502-145-21
; Sequence 21, Application US/10502145
; Publication No. US20050244406A1
; GENERAL INFORMATION:
; APPLICANT: MACKAY, CHARLES REAY
; TITLE OF INVENTION: Anti-C5ar antibodies and uses thereof
; FILE REFERENCES: RICH-032
; CURRENT APPLICATION NUMBER: US/10/502,145
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: USSN 60/350,961
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-502-145-21

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Query Match	62.0%;	Score 57;	DB 6;	Length 121;
Best Local Similarity	62.5%;	Pred. No. 0.0044;		
Matches 10; Conservative	2;	Mismatches 4;	Indels	

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QY      2 IYPGDSDTIYSPSFQG 17
      ||||| |:|
Db     51 IYPGDGDTKYNGKFKG 66
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RESULT 13
US-11-084-717-21
; Sequence 21, Application US/11084717
; Publication No. US20050260736A1
; GENERAL INFORMATION:
; APPLICANT: GEORGIOU, GEORGE
; APPLICANT: JEONG, KI-JUN
; APPLICANT: HARVEY, BARRETT R.
; APPLICANT: IYERSON, BRENT L.
; TITLE OF INVENTION: SELECTION OF BACTERIAL INNER-MEMBRANE ANCHOR POLYPEPTIDES
; FILE REFERENCE: UTSB:723JUS
; CURRENT APPLICATION NUMBER: US/11/084,717
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: 60/554,324
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: 10/620,278
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/396,058
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-084-717-21

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Query Match 62.0%; Score 57; DB 7; Length 247;


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Best Local Similarity 62.5%; Pred. No. 0.0092;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGSDTIYSPSQ 17
    ||||| ||| |. |. |. |
Db 179 IYPGSDTNYNGKFKG 194

RESULT 14
US-10-495-664-3
; Sequence 3, Application US/10495664
; Publication No. US2005024416A1
; GENERAL INFORMATION:
; APPLICANT: JUNG, GUNDRAM
; TITLE OF INVENTION: BISPECIFIC ANTI-CD28 ANTIBODY MOLECULE
; FILE REFERENCE: 034258-0801
; CURRENT APPLICATION NUMBER: US/10/495,664
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: PCT/EP02/12545
; PRIOR FILING DATE: 2002-11-09
; PRIOR APPLICATION NUMBER: DE 101 56 482.1
; PRIOR FILING DATE: 2001-11-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 3
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: protein construct
US-10-495-664-3

Query Match 62.0%; Score 57; DB 6; Length 543;
Best Local Similarity 62.5%; Pred. No. 0.021;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGSDTIYSPSQ 17
    ||||| ||| |. |. |
Db 337 IYPGSDTNYNGKFKG 352

RESULT 15
US-11-054-515-2088
; Sequence 2088, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2088
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2088

Query Match 60.9%; Score 56; DB 7; Length 248;
Best Local Similarity 75.0%; Pred. No. 0.013;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGSDTIYSPSQ 17
    ||||| ||| |. |. |
Db 51 IDPSDSTNYSPSQ 66

Search completed: December 3, 2005, 14:17:55
Job time : 1.97143 secs
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OM protein - protein search, using sw model

Run on: December 3, 2005, 14:10:00 ; Search time 198.384 Seconds
(without alignments)
256.916 Million cell updates/sec

Title: US-10-769-144-4

Perfect score: 621

Sequence: 1 EVQLVQSGAEVKPGESLR.....TRGDRGVYMGQGLTVTVSS 116

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	621	100.0	116	8 ADR46821	Adr46821 Human ant
3	621	100.0	411	8 ADR46829	Adr46829 Human pB1
4	621	100.0	468	8 ADR46819	Adr46819 Human ant
5	621	100.0	613	8 ADR46827	Adr46827 Human bet
6	560	90.2	117	8 ADP47223	Adp47223 Human pho
7	558.5	89.9	245	4 AAB67622	Aab67622 Human leu
8	558	89.9	117	8 ADP47094	Adp47094 Human pho
9	556	89.5	120	2 AAW27555	Aaw27555 Human ab
10	556	89.5	120	6 ABJ18677	Abj18677 Antibody
11	556	89.5	120	6 ABJ18720	Abj18720 Antibody
12	552.5	89.0	252	5 ABP45526	Abp45526 Human bly
13	552.5	89.0	252	7 ADG96353	Adg96353 Single ch
14	552.5	89.0	266	8 ADP69305	Adp69305 Human lun
15	552	88.9	117	8 ADP47229	Adp47229 Human pho
16	550.5	88.6	118	8 ADP47230	Adp47230 Human pho
17	550	88.6	224	6 ABR01533	Abro1533 Human ant
18	550	88.6	224	6 ABR01530	Abro1530 Human ant
19	550	88.6	226	6 ABR01522	Abro1522 Human ant
20	549.5	88.5	474	9 AEA12652	Aea12652 Heavy cha
21	549.5	88.5	474	9 AEA12653	Aea12653 Heavy cha
22	549.5	88.5	474	9 AEA18909	Aea18909 Variant h
23	549.5	88.5	474	9 AEA18908	Aea18908 Heavy cha
24	549.5	88.5	474	9 AEA18548	Aea18548 Heavy cha

25	549.5	88.5	474	9 AEA18549	Aea18549 Variant o
26	549.5	88.5	474	9 AEA10642	Aea10642 Human ant
27	549.5	88.5	474	9 AEA10641	Aea10641 Human ant
28	548.5	88.3	118	8 ADP47116	Adp47116 Human pho
29	548.5	88.3	118	8 ADP47219	Adp47219 Human pho
30	548.5	88.3	138	6 AAE37207	Aae37207 Human AB-
31	548.5	88.3	138	9 AEA16229	Aea16229 Anti-huma
32	548.5	88.3	245	4 AAB67621	Aab67621 Human leu
33	548	88.2	117	8 ADL70771	Adl70771 Anti-TNPa
34	548	88.2	224	6 ABR01528	Abro1528 Human ant
35	547	88.1	224	6 ABR01545	Abro1545 Human ant
36	546.5	88.0	118	8 ADP47098	Adp47098 Human pho
37	546.5	88.0	118	8 ADP47114	Adp47114 Human pho
38	546.5	88.0	118	8 ADP47092	Adp47092 Human pho
39	546.5	88.0	118	8 ADP47224	Adp47224 Human pho
40	546.5	88.0	119	9 ADZ42024	Adz42024 Ig H chai
41	545.5	87.8	118	8 ADP47228	Adp47228 Human pho
42	545	87.8	116	8 ADP22260	Adp22260 Human ant
43	544	87.6	116	8 ADP22194	Adp22194 Human ant
44	544	87.6	126	7 ADK18889	Adk18889 Anti-huma
45	544	87.6	224	6 ABR01527	Abro1527 Human ant

ALIGNMENTS

RESULT 1

AAM48005

ID AAM48005 standard; protein; 116 AA.

XX AAM48005;

DT 08-MAR-2002 (first entry)

DE Human monoclonal antibody B11 variable heavy chain protein.

XX Human; monoclonal antibody; B11; antigen binding portion; dendritic cell;
KW mannose receptor; growth; cytolysis; pathogen; virus; bacterium;
KW autoimmune disease; inflammatory disorder; rheumatoid arthritis;
KW multiple sclerosis; diabetes mellitus; immunomodulatory;
KW antiinflammatory; antirheumatic; antiarthritic; neuroprotective;
KW antidabetic; antianemic; endocrine; dermatological; antithyroid;
KW uropathic; ophthalmological; muscular.

XX Homo sapiens.

OS WO200185798-A2.

PN 15-NOV-2001.

PD 08-MAY-2001; 2001WO-US015114.

XX 08-MAY-2000; 2000US-0203126P.

PR 07-SEP-2000; 2000US-0230739P.

XX (MEDA-) MEDAREX INC.

PI Deo YM, Keler T;

XX WPI; 2002-089788/12.

DR N-PSDB; ABA05500.

XX New human monoclonal antibodies specific for dendritic cells, useful for
inhibiting growth or inducing cytolysis of a dendritic cell and treating
or preventing a dendritic cell mediated disease, e.g., autoimmune
disorders.

PS Example 2; Fig 13; 95pp; English.

XX The invention relates to human monoclonal antibodies or their antigen
binding portions that specifically bind to dendritic cells and has one or
more of the following characteristics: (a) a binding affinity constant to
a dendritic cell of at least about 10 to the power 7 M-1; (b) the ability

CC to opsonise a dendritic cell; (c) the ability to internalise after
CC binding to dendritic cells; or (d) the ability to activate dendritic
CC cells. The isolated human monoclonal antibody or its antigen binding
CC portion may also have any of the following characteristics: (a) mediates
CC cytotoxicity of dendritic cells in the presence of human effector cells; or
CC (b) inhibits growth of dendritic cells. The antibodies or its antigen
CC binding portion, binds to and blocks the human mannose receptor on
CC dendritic cells. The antibodies have immunomodulatory, antiinflammatory,
CC antirheumatic, antiarthritic, neuroprotective, antidiabetic, antianemic,
CC endocrine, dermatological, antithyroid, uropathic, ophthalmological and
CC muscular activity. The antibodies or their antigen-binding fragments are
CC useful for inhibiting growth of a dendritic cell, inducing cytotoxicity of a
CC dendritic cell, treating or preventing a dendritic cell mediated disease,
CC detecting the presence of a dendritic cell, targeting an antigen to a
CC dendritic cell and preventing binding of a pathogen (a virus or a
CC bacterium) to human mannose receptor on dendritic cells. In particular,
CC the antibodies may be used to treat, autoimmune disease, graft versus
CC host disease, immune system or inflammatory disorders (e.g. rheumatoid
CC arthritis), multiple sclerosis, diabetes mellitus, myasthenia gravis,
CC pernicious anaemia, Addison's disease, lupus erythematosus, Reiter's
CC syndrome and Graves disease. The present sequence is that of the human
CC monoclonal antibody B11 variable heavy chain, useful to the invention
XX
SQ Sequence 116 AA;

Query Match 100.0%; Score 621; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 7.2e-50;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EVQLVQSGAEVKPKGESLRISCKGSGDSFTTYWIGVWRQMPKGLWGMGIYPGDSDTIY 60
Db 1 EVQLVQSGAEVKPKGESLRISCKGSGDSFTTYWIGVWRQMPKGLWGMGIYPGDSDTIY 60
Qy 61 SPSPQGGVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVYWGQGLTVTVSS 116
Db 61 SPSPQGGVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVYWGQGLTVTVSS 116

RESULT 2
ADR46821
ID ADR46821 standard; protein; 116 AA.

XX ADR46821;
XX
DT 18-NOV-2004 (first entry)
DE Human antibody B11 heavy chain variable region protein SEQ ID NO:4.
KW molecular conjugate; monoclonal antibody; human antigen presenting cell;
KW antigen presenting cell; APC; human; beta human chorionic gonadotropin;
KW betahCG; beta chorionic gonadotropin; antibody;
KW T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
KW immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
KW CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
KW melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
KW antibody B11; heavy chain variable region.

XX Homo sapiens.
XX WO2004074432-A2.
XX
PD 02-SEP-2004.
XX
PP 30-JAN-2004; 2004WO-US002725.
XX
PP 31-JAN-2003; 2003US-0443979P.
XX
XX (MEDA-) MEDAREX INC.
XX
XX Keler T, Endres M, He L, Ramakrishna V;
XX WPI, 2004-635555/61.
XX
DR N-PSDB; ADR46820.

XX New molecular conjugate having a monoclonal antibody that binds to human
PT APCs linked to a beta human chorionic gonadotropin, useful for inducing a
PT cytotoxic T cell response in cancers and infectious diseases.
XX
PS Claim 11; SEQ ID NO 4; 82pp; English.

XX The present invention describes a molecular conjugate comprising a
CC monoclonal antibody that binds to human antigen presenting cells (APCs)
CC linked to beta human chorionic gonadotropin (betahCG), where the antibody
CC comprises a heavy and/or light chain variable region derived from a human
CC VHS-51 or VK-L15 germline sequence with the 98 or 95 amino acid sequences
CC of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
CC described: (1) a molecular conjugate comprising a human antibody heavy
CC chain and a human antibody light chain, where either or both chains are
CC linked to betahCG; (2) a molecular conjugate comprising a human single
CC chain antibody that binds to human APCs linked to betahCG, where the
CC conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
CC (ADR46829); (3) a composition comprising any of the molecular conjugates
CC as described above, and a carrier, optionally in combination with an
CC adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
CC against betahCG, comprising contacting any of the molecular conjugates
CC described above with APCs such that the antigen is processed and
CC presented to T cells in a manner which induces or enhances a T cell-
CC mediated response against the antigen; (5) immunising a subject
CC comprising administering any of the molecular conjugates described above,
CC optionally in combination with an adjuvant, a cytokine which stimulates
CC proliferation of dendritic cells and/or an immunostimulatory agent; and
CC (6) inducing or enhancing a cytotoxic T cell response against an antigen,
CC comprising forming a conjugate of the antigen and a monoclonal antibody
CC which binds to APCs, and contacting the conjugate either in vivo or ex
CC vivo with APCs such that the antigen is internalised, processed and
CC presented to T cells in a manner which induces or enhances a cytotoxic T
CC cell response against the antigen. The molecular conjugate has
CC cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
CC virucide and antimalarial activities, and can be used as a CD8 agonist,
CC and in vaccines. The methods and compositions of the present invention
CC are useful for inducing a cytotoxic T cell response, and in particular
CC for treating autoimmune disorders, cancers and infectious diseases by
CC eliciting a potent antigen-specific cytotoxic T lymphocyte response,
CC including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
CC herpes. The present sequence represents a human antibody B11 heavy chain
CC variable region, which is used in the exemplification of the present
XX invention.

XX Sequence 116 AA;

Query Match 100.0%; Score 621; DB 8; Length 116;
Best Local Similarity 100.0%; Pred. No. 7.2e-50;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EVQLVQSGAEVKPKGESLRISCKGSGDSFTTYWIGVWRQMPKGLWGMGIYPGDSDTIY 60
Db 1 EVQLVQSGAEVKPKGESLRISCKGSGDSFTTYWIGVWRQMPKGLWGMGIYPGDSDTIY 60
Qy 61 SPSPQGGVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVYWGQGLTVTVSS 116
Db 61 SPSPQGGVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVYWGQGLTVTVSS 116

RESULT 3
ADR46829
ID ADR46829 standard; protein; 411 AA.

XX ADR46829;
XX
DT 18-NOV-2004 (first entry)
DE Human pB11-betahCG molecular conjugate protein SEQ ID NO:12.
KW molecular conjugate; monoclonal antibody; human antigen presenting cell;
KW antigen presenting cell; APC; human; beta human chorionic gonadotropin;
KW betahCG; beta chorionic gonadotropin; antibody;

KW T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
KW immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
KW CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
KW melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
KW antibody B11; pB11-betahCG molecular conjugate; fusion protein.
XX
OS Homo sapiens.
OS Synthetic.
XX WO2004074432-A2.
XX
XX
XX 02-SEP-2004.
XX
XX 30-JAN-2004; 2004WO-US002725.
XX
XX 31-JAN-2003; 2003US-0443979P.
XX
XX (MEDA-) MEDAREX INC.
XX
XX Keler T, Endres M, He L, Ramakrishna V;
XX
XX WPI; 2004-635555/61.
XX N-PSDB; ADR46828.
XX
XX New molecular conjugate having a monoclonal antibody that binds to human
XX APCs linked to a beta human chorionic gonadotropin, useful for inducing a
XX cytotoxic T cell response in cancers and infectious diseases.
XX
XX Claim 16; SEQ ID NO 12; 82pp; English.
XX
XX The present invention describes a molecular conjugate comprising a
XX monoclonal antibody that binds to human antigen presenting cells (APCs)
XX linked to beta human chorionic gonadotropin (betahCG), where the antibody
XX comprises a heavy and/or light chain variable region derived from a human
XX VHS-51 or Vκ-L15 germline sequence with the 98 or 95 amino acid sequences
XX of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
XX described: (1) a molecular conjugate comprising a human antibody heavy
XX chain and a human antibody light chain, where either or both chains are
XX linked to betahCG; (2) a molecular conjugate comprising a human single
XX chain antibody that binds to human APCs linked to betahCG, where the
XX conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
XX (ADR46829); (3) a composition comprising any of the molecular conjugates
XX as described above, and a carrier, optionally in combination with an
XX adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
XX against betahCG, comprising contacting any of the molecular conjugates
XX described above with APCs such that the antigen is processed and
XX presented to T cells in a manner which induces or enhances a T cell-
XX mediated response against the antigen; (5) immunising a subject
XX comprising administering any of the molecular conjugates described above,
XX optionally in combination with an adjuvant, a cytokine which stimulates
XX proliferation of dendritic cells and/or an immunostimulatory agent; and
XX (6) inducing or enhancing a cytotoxic T cell response against an antigen,
XX comprising forming a conjugate of the antigen and a monoclonal antibody
XX which binds to APCs, and contacting the conjugate either in vivo or ex
XX vivo with APCs such that the antigen is internalised, processed and
XX presented to T cells in a manner which induces or enhances a cytotoxic T
XX cell response against the antigen. The molecular conjugate has
XX cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
XX virucide and antimalarial activities, and can be used as a CD8 agonist,
XX and in vaccines. The methods and compositions of the present invention
XX are useful for inducing a cytotoxic T cell response, and in particular
XX for treating autoimmune disorders, cancers and infectious diseases by
XX eliciting a potent antigen-specific cytotoxic T lymphocyte response,
XX including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
XX herpes. The present sequence represents a human pB11-betahCG molecular
XX conjugate, which is used in the exemplification of the present invention.

SQ Sequence 411 AA;

Query Match 100.0%; Score 621; DB 8; Length 411;
Best Local Similarity 100.0%; Pred. No. 2.7e-49;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGSFYYTWIGWVRQMPGKGLEWGIYPGSDTIY 60
Db 142 EVQLVQSGAEVKKPGESLRISCKGSGSFYYTWIGWVRQMPGKGLEWGIYPGSDTIY 201
Qy 61 SPSPQGOVTTISADKSIISTAYLQWSSSLKASDTAMYCYCTRGRGVGYWGQGLTVTVSS 116
Db 202 SPSPQGOVTTISADKSIISTAYLQWSSSLKASDTAMYCYCTRGRGVGYWGQGLTVTVSS 257
RESULT 4
ID ADR46819
XX ADR46819 standard; protein; 468 AA.
XX AC ADR46819;
XX
XX 18-NOV-2004 (first entry)
XX
XX Human antibody B11 heavy chain variable region protein SEQ ID NO:2.
XX
XX molecular conjugate; monoclonal antibody; human antigen presenting cell;
XX antigen presenting cell; APC; human; beta human chorionic gonadotropin;
XX betahCG; beta chorionic gonadotropin; antibody;
XX T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
XX immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
XX CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
XX melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
XX antibody B11; heavy chain variable region.
XX
XX Homo sapiens.
XX
XX WO2004074432-A2.
XX
XX 02-SEP-2004.
XX
XX 30-JAN-2004; 2004WO-US002725.
XX
XX 31-JAN-2003; 2003US-0443979P.
XX (MEDA-) MEDAREX INC.
XX
XX Keler T, Endres M, He L, Ramakrishna V;
XX
XX WPI; 2004-635555/61.
XX N-PSDB; ADR46818.
XX
XX New molecular conjugate having a monoclonal antibody that binds to human
XX APCs linked to a beta human chorionic gonadotropin, useful for inducing a
XX cytotoxic T cell response in cancers and infectious diseases.
XX
XX Claim 13; SEQ ID NO 2; 82pp; English.
XX
XX The present invention describes a molecular conjugate comprising a
XX monoclonal antibody that binds to human antigen presenting cells (APCs)
XX linked to beta human chorionic gonadotropin (betahCG), where the antibody
XX comprises a heavy and/or light chain variable region derived from a human
XX VHS-51 or Vκ-L15 germline sequence with the 98 or 95 amino acid sequences
XX of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
XX described: (1) a molecular conjugate comprising a human antibody heavy
XX chain and a human antibody light chain, where either or both chains are
XX linked to betahCG; (2) a molecular conjugate comprising a human single
XX chain antibody that binds to human APCs linked to betahCG, where the
XX conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
XX (ADR46829); (3) a composition comprising any of the molecular conjugates
XX as described above, and a carrier, optionally in combination with an
XX adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
XX against betahCG, comprising contacting any of the molecular conjugates
XX described above with APCs such that the antigen is processed and
XX presented to T cells in a manner which induces or enhances a T cell-
XX mediated response against the antigen; (5) immunising a subject
XX comprising administering any of the molecular conjugates described above,
XX optionally in combination with an adjuvant, a cytokine which stimulates
XX proliferation of dendritic cells and/or an immunostimulatory agent; and
XX (6) inducing or enhancing a cytotoxic T cell response against an antigen,

comprising forming a conjugate of the antigen and a monoclonal antibody which binds to APCs, and contacting the conjugate either in vivo or ex vivo with APCs such that the antigen is internalised, processed and presented to T cells in a manner which induces or enhances a cytotoxic T cell response against the antigen. The molecular conjugate has cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic, virucide and antimalarial activities, and can be used as a CD8 agonist, and in vaccines. The methods and compositions of the present invention are useful for inducing a cytotoxic T cell response, and in particular for treating autoimmune disorders, cancers and infectious diseases by eliciting a potent antigen-specific cytotoxic T lymphocyte response, including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and herpes. The present sequence represents a human antibody B11 heavy chain variable region, which is used in the exemplification of the present invention.

XX Sequence 468 AA;

Query Match 100.0%; Score 621; DB 8; Length 468;
Best Local Similarity 100.0%; Pred. No. 3.1e-49;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKPGESLRISCKGSGDSFTTYTWIGVRQMPKGLWNGIIPGDSDTIY 60

Db 20 EVQLVQSGAEVKPGESLRISCKGSGDSFTTYTWIGVRQMPKGLWNGIIPGDSDTIY 79

Qy 61 SPSPGQGVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVYWGQGLTIVTSS 116

Db 80 SPSPGQGVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVYWGQGLTIVTSS 135

RESULT 5

ADP46827
ID ADP46827 standard; protein; 613 AA.

XX AC ADP46827;

XX DT 18-NOV-2004 (first entry)

XX DE Human betahCG-B11 molecular conjugate protein SEQ ID NO:10.

XX molecular conjugate; monoclonal antibody; human antigen presenting cell;
XX antigen presenting cell; APC; human; beta human chorionic gonadotropin;
XX betahCG; beta chorionic gonadotropin; antibody;
XX T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
XX immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
XX CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
XX melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
XX antibody B11; betahCG-B11 molecular conjugate; fusion protein.

XX Homo sapiens.

OS Synthetic.

XX WO2004074432-A2.

XX PD 02-SEP-2004.

XX PF 30-JAN-2004; 2004WO-US002725.

XX PR 31-JAN-2003; 2003US-0443979P.

XX PA (MEDA-) MEDAREX INC.

XX PI Keler T, Endres M, He L, Ramakrishna V;

XX DR WPI; 2004-635555/61.

XX DR N-PSDB; ADP46826.

XX New molecular conjugate having a monoclonal antibody that binds to human
XX APCs linked to a beta human chorionic gonadotropin, useful for inducing a
XX cytotoxic T cell response in cancers and infectious diseases.

XX Example 1; SEQ ID NO 10; 82pp; English.

XX The present invention describes a molecular conjugate comprising a
XX monoclonal antibody that binds to human antigen presenting cells (APCs)
XX linked to beta human chorionic gonadotropin (betahCG), where the antibody
XX comprises a heavy and/or light chain variable region derived from a human
XX VH5-51 or VK-L15 germline sequence with the 98 or 95 amino acid sequences
XX of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
XX described: (1) a molecular conjugate comprising a human antibody heavy
XX chain and a human antibody light chain, where either or both chains are
XX linked to betahCG; (2) a molecular conjugate comprising a human single
XX chain antibody that binds to human APCs linked to betahCG, where the
XX conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
XX (ADR46829); (3) a composition comprising any of the molecular conjugates
XX as described above, and a carrier, optionally in combination with an
XX adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
XX against betahCG, comprising contacting any of the molecular conjugates
XX described above with APCs such that the antigen is processed and
XX presented to T cells in a manner which induces or enhances a T cell-
XX mediated response against the antigen; (5) immunising a subject
XX comprising administering any of the molecular conjugates described above,
XX optionally in combination with an adjuvant, a cytokine which stimulates
XX proliferation of dendritic cells and/or an immunostimulatory agent; and
XX (6) inducing or enhancing a cytotoxic T cell response against an antigen,
XX comprising forming a conjugate of the antigen and a monoclonal antibody
XX which binds to APCs, and contacting the conjugate either in vivo or ex
XX vivo with APCs such that the antigen is internalised, processed and
XX presented to T cells in a manner which induces or enhances a cytotoxic T
XX cell response against the antigen. The molecular conjugate has
XX cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
XX virucide and antimalarial activities, and can be used as a CD8 agonist,
XX and in vaccines. The methods and compositions of the present invention
XX are useful for inducing a cytotoxic T cell response, and in particular
XX for treating autoimmune disorders, cancers and infectious diseases by
XX eliciting a potent antigen-specific cytotoxic T lymphocyte response,
XX including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
XX herpes. The present sequence represents a human betahCG-B11 molecular
XX conjugate, which is used in the exemplification of the present invention.

XX Sequence 613 AA;

Query Match 100.0%; Score 621; DB 8; Length 613;
Best Local Similarity 100.0%; Pred. No. 4.1e-49;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKPGESLRISCKGSGDSFTTYTWIGVRQMPKGLWNGIIPGDSDTIY 60

Db 20 EVQLVQSGAEVKPGESLRISCKGSGDSFTTYTWIGVRQMPKGLWNGIIPGDSDTIY 79

Qy 61 SPSPGQGVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVYWGQGLTIVTSS 116

Db 80 SPSPGQGVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVYWGQGLTIVTSS 135

RESULT 6

ADP47223

ID ADP47223 standard; protein; 117 AA.

XX AC ADP47223;

XX DT 09-SEP-2004 (first entry)

XX DE Human phospholipase A2-specific monoclonal antibody heavy chain #21.

XX human; monoclonal antibody; phospholipase A2; PLA2;

XX inflammatory disorder; degenerative disorder;

XX joint inflammatory reaction; skin inflammatory reaction;

XX blood vessels inflammatory reaction; arthritis; psoriasis; asthma;

XX Alzheimer's disease; atherosclerosis; restenosis; heavy chain.

XX Homo sapiens.

XX WO2004050850-A2.

XX PN

PD 17-JUN-2004.
 XX
 PF 02-DEC-2003; 2003WO-US038234.
 XX
 XX
 PR 02-DEC-2002; 2002US-0430724P.
 XX
 XX (ABGE-) ABGENIX INC.
 XX (LEXI-) LEXICON GENETICS INC.
 PA Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;
 XX Jia X, Nocerini MR;
 PI WPI; 2004-461119/43.
 XX
 DR New human monoclonal antibody that binds to phospholipase A2 (PLA2),
 XX useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
 PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.
 PT
 XX Example 5; SEQ ID NO 139; 128pp; English.
 PS
 XX The invention comprises a human monoclonal antibody that binds to
 CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is
 CC useful in the preparation of a medicament for the treatment of
 CC inflammatory and degenerative disorders stemming from inflammatory
 CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
 CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
 CC amino acid sequence represents the heavy chain from a monoclonal antibody
 CC that is specific for the human phospholipase A2 (PLA2) enzyme.
 XX
 XX Sequence 117 AA;
 SQ
 Query Match 90.2%; Score 560; DB 8; Length 117;
 Best Local Similarity 91.4%; Pred. No. 3.3e-44;
 Matches 106; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 QY 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTWIGWVRQMPGKGLEWMGIYPGSDTIY 60
 DB 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTWIGWVRQMPGKGLEWMGIYPGSDTRY 60
 QY 61 SPSPFGQVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDGRGVGYGGTGLTVTSS 116
 DB 61 SPSPFGQVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDGRGVGYGGTGLTVTSS 116
 RESULT 7
 AAB67622
 ID AAB67622 standard; protein; 245 AA.
 XX
 AC AAB67622;
 XX
 XX 29-MAY-2001 (first entry)
 XX
 DE Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6_6.
 XX
 XX Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;
 KW miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200114558-A1.
 XX
 XX 01-MAR-2001.
 XX
 PF 28-AUG-2000; 2000WO-EP008388.
 XX
 XX 26-AUG-1999; 99EP-00116691.
 XX
 XX (MORP-) MORPHOSYS AG.
 XX
 PI Kretzschmar T, Tesar M, Marget M, Kroenke M;
 XX WPI; 2001-218451/22.
 XX
 XX
 PT Novel isolated human immunoglobulin or functional immunoglobulin fragment
 specific for human leukocyte antigen Cw6, useful for treatment of humans
 and for human leukocyte antigen phenotyping.
 XX
 XX Claim 3; Fig 1; 23pp; English.
 XX
 CC AAB67617-23 represent single chain antibody (scFv) fragments which are
 specific for human leukocyte antigen (HLA)-Cw6. The fragments are derived
 from a synthetic human combinatorial antibody library based on molecular
 consensus frameworks and CDRs randomised with trinucleotides. The
 specification describes a human immunoglobulin fragments specific for HLA
 -Cw6. The HLA-Cw6 serotype is considered highly relevant in studies of
 natural killer cell silencing as well as miscarriages. HLA-Cw6
 demonstrates a disequilibrium in some recurrent abortions. Psoriasis may
 also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin fragments are
 useful for the preparation of a pharmaceutical for the treatment of
 humans. They are also useful for HLA phenotyping
 XX
 XX Sequence 245 AA;
 SQ
 Query Match 89.9%; Score 558.5; DB 4; Length 245;
 Best Local Similarity 91.5%; Pred. No. 1e-43;
 Matches 107; Conservative 3; Mismatches 6; Indels 1; Gaps 1;
 QY 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTWIGWVRQMPGKGLEWMGIYPGSDTIY 60
 DB 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTWIGWVRQMPGKGLEWMGIYPGSDTRY 60
 QY 61 SPSPFGQVTTISADKSIISTAYLQWSSLKASDTAMYCTRGD-RGVGYGGTGLTVTSS 116
 DB 61 SPSPFGQVTTISADKSIISTAYLQWSSLKASDTAMYCTRGD-RGVGYGGTGLTVTSS 117
 RESULT 8
 ADP47094
 ID ADP47094 standard; protein; 117 AA.
 XX
 AC ADP47094;
 XX
 XX 09-SEP-2004 (first entry)
 XX
 DE Human phospholipase A2-specific monoclonal antibody heavy chain #4.
 XX
 KW human; monoclonal antibody; phospholipase A2; PLA2;
 KW inflammatory disorder; degenerative disorder;
 KW joint inflammatory reaction; skin inflammatory reaction;
 KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
 KW Alzheimer's disease; atherosclerosis; restenosis; heavy chain.
 XX
 OS Homo sapiens.
 XX
 XX WO2004050850-A2.
 XX
 XX 17-JUN-2004.
 XX
 PF 02-DEC-2003; 2003WO-US038234.
 XX
 PR 02-DEC-2002; 2002US-0430724P.
 XX
 XX (ABGE-) ABGENIX INC.
 XX (LEXI-) LEXICON GENETICS INC.
 PA Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;
 XX Jia X, Nocerini MR;
 PI WPI; 2004-461119/43.
 XX
 DR New human monoclonal antibody that binds to phospholipase A2 (PLA2),
 XX useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
 PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.
 PT
 XX Claim 1; SEQ ID NO 9; 128pp; English.
 XX

CC The invention comprises a human monoclonal antibody that binds to
CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is
CC useful in the preparation of a medicament for the treatment of
CC inflammatory and degenerative disorders stemming from inflammatory
CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
CC amino acid sequence represents the heavy chain from a monoclonal antibody
CC that is specific for the human phospholipase A2 (PLA2) enzyme.

XX
XX
SQ Sequence 117 AA;

Query Match 89.9%; Score 558; DB 8; Length 117;
Best Local Similarity 91.4%; Pred. No. 5.1e-44;
Matches 106; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGSFSTTYWIGVWRQMPGKGLWNGIIYPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGSFSTTYWIGVWRQMPGKGLWNGIIYPGDSDTIY 60

Qy 61 SPSPQGGVTTISADKSIISTAYLQWSSLSKASDTAMYCTR-----GDRGVDMQGGTLVTYSS 116

Db 61 SPSPQGGVTTISADKSIISTAYLQWSSLSKASDTAMYCTR-----GDRGVDMQGGTLVTYSS 116

RESULT 9

AAW27555
ID AAW27555 standard; protein; 120 AA.

XX
XX AAW27555;

DT 23-JAN-1998 (first entry)

XX Human Ab heavy chain variable region VH5 consensus.

XX Human; antibody; preparation; library; VH5; variable region; heavy chain;
XX consensus.

XX Homo sapiens.

XX WO9708320-A1.

XX 06-MAR-1997.

XX 19-AUG-1996; 96WO-EP003647.

XX 18-AUG-1995; 95EP-00113021.

XX (MORP-) MORPHOSYS GBS PROTEINOPTIMIERUNG MBH.

XX Knappik A, Pack P, Ilag V, Ge L, Moroney S, Plueckthun A;

XX WPI; 1997-179277/16.

XX N-ESDB; AAT87953.

XX Preparation of human derived antibody gene library - using synthetic
XX consensus sequences, and signal consensus antibody gene as universal
XX framework for highly diverse antibody libraries.

XX Example 1; Fig 5F; 436pp; English.

XX The present sequence is the human antibody heavy chain variable region
XX synthetic sequence VH5, used in the preparation of a human derived
XX antibody gene library

XX Sequence 120 AA;

Query Match 89.5%; Score 556; DB 2; Length 120;
Best Local Similarity 89.2%; Pred. No. 8e-44;
Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGSFSTTYWIGVWRQMPGKGLWNGIIYPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGSFSTTYWIGVWRQMPGKGLWNGIIYPGDSDTIY 60

Qy 61 SPSPQGGVTTISADKSIISTAYLQWSSLSKASDTAMYCTR-----GDRGVDMQGGTLVTYSS 116
Db 61 SPSPQGGVTTISADKSIISTAYLQWSSLSKASDTAMYCTR-----GDRGVDMQGGTLVTYSS 120

RESULT 10

ABJ18677
ID ABJ18677 standard; protein; 120 AA.

XX
XX ABJ18677;

DT 06-MAR-2003 (first entry)

XX Antibody library related heavy variable chain protein region SEQ ID No 6.

XX Library; recombinant antibody; clustering variable region; in silico;
XX immunogenecity; antibody therapeutic.

XX Unidentified.

XX WO200284277-A1.

XX 24-OCT-2002.

XX 17-APR-2002; 2002WO-US012202.

XX 17-APR-2001; 2001US-0284407P.

XX (ABMA-) ABMAXIS INC.

XX Luo P;

XX WPI; 2003-093043/08.

XX Constructing a library of recombinant antibodies useful as source of
XX antibody candidates for screening antigens comprises clustering variable
XX regions of antibodies having known 3-dimensional structures into
XX structural ensembles.

XX Disclosure; Page 102-103; 119pp; English.

XX The invention relates to a novel method for the construction of a library
XX of recombinant antibodies. The novel method comprises clustering variable
XX regions of a collection of antibodies having known 3D structures into at
XX least two families of structural ensembles, each comprising at least two
XX different antibody sequences but with substantially identical main chain
XX conformations. The method is useful for constructing a library of
XX artificial antibodies in silico which provides a structurally diverse and
XX yet functionally more relevant source of antibody candidates which can
XX then be screened for binding a wide variety of target molecules,
XX including small molecules, and biomacromolecules such as proteins,
XX peptides and nucleic acids. The libraries constructed are useful as a
XX source of antibody candidates for further screening for novel antibodies
XX with high affinity against a wide range of antigens and having no or
XX minimum immunogenicity to human subjects treated with antibody
XX therapeutics. This sequence represents a protein region of an antibody
XX relating to the novel antibody library construction method of the
XX invention

XX Sequence 120 AA;

Query Match 89.5%; Score 556; DB 6; Length 120;
Best Local Similarity 89.2%; Pred. No. 8e-44;
Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGSFSTTYWIGVWRQMPGKGLWNGIIYPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGSFSTTYWIGVWRQMPGKGLWNGIIYPGDSDTIY 60

Qy 61 SPSPQGGVTTISADKSIISTAYLQWSSLSKASDTAMYCTR-----GDRGVDMQGGTLVTYSS 116
Db 61 SPSPQGGVTTISADKSIISTAYLQWSSLSKASDTAMYCTR-----GDRGVDMQGGTLVTYSS 120


```

Qy      112 VTVSS 116
Db      121 VTVSS 125

RESULT 13
ADG96353
XX      ADG96353 standard; protein; 252 AA.
AC      ADG96353;
XX
DT      11-MAR-2004 (first entry)
XX
DE      Single chain antibody that immunospecifically binds Blys SeqID 1537.
XX
KW      antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KW      B cell proliferation; differentiation; scFv; myasthenia gravis;
KW      multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW      carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KW      antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
OS      Unidentified.
XX
PN      WO2003055979-A2.
XX
PD      10-JUL-2003.
XX
PF      14-NOV-2002; 2002WO-US036496.
XX
PR      16-NOV-2001; 2001US-0331469P.
PR      19-DEC-2001; 2001US-0340817P.
XX
PA      (HUMA-) HUMAN GENOME SCI INC.
XX
PI      Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX      WPI; 2003-505530/47.
XX
PT      Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT      (Blys), useful for detecting and treating diseases or disorders e.g.
PT      rheumatoid arthritis, asthma and leukemia.
XX
PS      Example 1; SEQ ID NO 1537; 394pp; English.
XX
CC      This invention relates to novel antibodies that immunospecifically bind
CC      to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC      chromosome 13q34 and encodes a protein that is a member of the tumour
CC      necrosis factor superfamily and induces both in vivo and in vitro B cell
CC      proliferation and differentiation. Specifically, it refers to single
CC      chain antibody molecules (scFvs) derived, preferably, from the variable
CC      heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC      fragment thereof, of either human, murine, rat or monkey Blys. The
CC      present invention refers to the use of such antibodies in various methods
CC      for the detection, diagnosis and prognosis of diseases related to the
CC      aberrant expression or inappropriate function of Blys or its receptor. As
CC      such, these compositions are useful for identifying immune disorders
CC      including myasthenia gravis and multiple sclerosis, inflammatory
CC      disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC      as AIDS and proliferative disorders including leukaemia, carcinoma and
CC      lymphoma. Accordingly, they can be described as exhibiting various
CC      activities such as antirheumatic, antiarthritic, neuroprotective,
CC      antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
CC      polypeptide sequence is a single chain antibody that binds Blys of the
CC      invention. NOTE: The sequence data for this patent did not form part of
CC      the printed specification, but was obtained in electronic format
CC      directly from WIPO at ftp.wipo.int/pub/published pct_sequences.
XX
SQ      Sequence 252 AA;

Query Match      89.0%; Score 552.5; DB 7; Length 252;
Best Local Similarity 84.8%; Pred. No. 3.7e-43;
Matches 106; Conservative 4; Mismatches 6; Indels 9; Gaps 1;

Qy      1 EVQLVQSGAEVKKPGESLRISCKSGDSFTYYIGWVRQMPGKLEWMGIYPGSDTIY 60
Db      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 QVQLVQSGAEVKKPGESLRISCKSGDSFTSYIGWVRQMPGKLEWMGIYPGSDTRY 60

RESULT 14
ADP69305
XX      ADP69305 standard; protein; 266 AA.
AC      ADP69305;
XX
DT      26-FEB-2004 (first entry)
XX
DE      Human lung specific protein sequence SEQ ID NO:62.
XX
KW      human; lung specific nucleic acid; lung specific protein; lung cancer;
KW      cytostatic; gene therapy.
XX
OS      Homo sapiens.
XX
PN      WO2003102137-A2.
XX
PD      11-DEC-2003.
XX
PF      30-MAY-2003; 2003WO-US016810.
XX
PR      31-MAY-2002; 2002US-0385301P.
XX
PA      (DIAD-) DIADEXUS INC.
XX
PI      Chen S, Macina RA, Sun Y, Liu C, Turner LR;
XX      WPI; 2004-053457/05.
XX
PT      New human lung specific nucleic acid, useful for preparing a composition
PT      for diagnosing or treating lung cancer.
XX
PS      Claim 11; SEQ ID NO 62; 221pp; English.
XX
CC      The present invention describes a human lung specific nucleic acid
CC      molecule. Also described: (1) a method for determining the presence of a
CC      lung specific nucleic acid (LSNA) in a sample; (2) a vector comprising
CC      the nucleic acid molecule; (3) a host cell comprising the vector; (4) a
CC      method for producing a polypeptide encoded by the nucleic acid molecule;
CC      (5) a polypeptide encoded by the nucleic acid molecule; (6) an antibody
CC      or its fragment that specifically binds to the polypeptide; (7) a method
CC      for determining the presence of a lung specific protein in a sample; (8)
CC      a method for diagnosing and monitoring the presence and metastases of
CC      lung cancer in a patient; (9) a kit for detecting a risk of cancer or
CC      presence of cancer in a patient comprising a means for determining the
CC      presence of the nucleic acid molecule or polypeptide in a sample of a
CC      patient; (10) a method of treating a patient with lung cancer; and (11) a
CC      vaccine comprising the polypeptide or the nucleic acid encoding the
CC      polypeptide. Human LSNA molecules and related proteins have cytostatic
CC      activity, and can be used in gene therapy. They are useful for preparing
CC      a composition for diagnosing or treating lung cancer. The present
CC      sequence represents a human lung specific protein, which is used in the
CC      exemplification of the present invention.
XX
SQ      Sequence 266 AA;

Query Match      89.0%; Score 552.5; DB 8; Length 266;
Best Local Similarity 88.4%; Pred. No. 3.9e-43;
Matches 107; Conservative 2; Mismatches 7; Indels 5; Gaps 1;

```

QY 1 EVLVQSGAEVKKPGESLRISCKGSDSFTTWIGWVRQMPKGLWNGIIPGDSDTIY 60
Db 12 EVLVQSGAEVKKPGESLRISCKGSGYSFTSYWIGWVRQMPKGLWNGIIPGDSDTY 71
QY 61 SPSFGQVTTISADKSIISTAYLQWSSLKASDTAMYCTR-----GDRGVDYWGQGLTVTVS 115
Db 72 SPSFGQVTTISADKSIISTAYLQWSSLKASDTAMYCTRPIAVAGHYFYDYWGQGLTVTVS 131

QY 116 S 116

Db 132 S 132

RESULT 15

ADP47229

ID ADP47229 standard; protein; 117 AA.

AC ADP47229;

XX 09-SEP-2004 (first entry)

XX Human phospholipase A2-specific monoclonal antibody heavy chain #27.

XX human; monoclonal antibody; phospholipase A2; PLA2;

KW inflammatory disorder; degenerative disorder;

KW joint inflammatory reaction; skin inflammatory reaction;

KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;

KW Alzheimer's disease; atherosclerosis; restenosis; heavy chain.

XX Homo sapiens.

XX WO2004050850-A2.

XX 17-JUN-2004.

XX 02-DEC-2003; 2003WO-US038234.

XX 02-DEC-2002; 2002US-0430724P.

XX (ABGE-) AGENIX INC.

XX (LEXI-) LEXICON GENETICS INC.

XX Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;

XX Jia X, Nocerini MR;

XX WPI; 2004-461119/43.

XX New human monoclonal antibody that binds to phospholipase A2 (PLA2),
PT useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.

PS Example 5; SEQ ID NO 144; 128pp; English.

XX The invention comprises a human monoclonal antibody that binds to
CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is
CC useful in the preparation of a medicament for the treatment of
CC inflammatory and degenerative disorders stemming from inflammatory
CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
CC amino acid sequence represents the heavy chain from a monoclonal antibody
CC that is specific for the human phospholipase A2 (PLA2) enzyme.

XX Sequence 117 AA;

Query Match 88.9%; Score 552; DB 8; Length 117;

Best Local Similarity 89.7%; Pred. NO. 1.8e-43;

Matches 104; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 EVLVQSGAEVKKPGESLRISCKGSDSFTTWIGWVRQMPKGLWNGIIPGDSDTIY 60

Db 1 EVLVQSGAEVKKPGESLRISCKGSGYSFTSYWIGWVRQMPKGLWNGIIPGDSDTY 60

QY 61 SPSFGQVTTISADKSIISTAYLQWSSLKASDTAMYCTRGRGVDYWGQGLTVTVS 116

Db 61 SPSFGQVTTISADKSIISTAYLQWSSLKASDTAMYCARXXXAFDIWGQGTWTVTVSS 116

Search completed: December 3, 2005, 14:25:01
Job time : 200.384 secs

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OM protein - protein search, using sw model

Run on: December 3, 2005, 14:11:48 ; Search time 204.539 Seconds
(without alignments)
400.126 Million cell updates/sec

Title: US-10-769-144-4

Perfect score: 621

Sequence: 1 EVQLVQSGAEVKKPGESLR.....TRGDRGVYMGQGLTVTVSS 116

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	434	69.9	475	Q5RE17_PONPY	Q5RE17 pongo pygma
2	389	62.6	124	Q9UL92_HUMAN	Q9UL92 homo sapien
3	381.5	61.4	119	Q9UL94_HUMAN	Q9UL94 homo sapien
4	379	61.0	118	Q921C4_MOUSE	Q921C4 mus musculus
5	379	61.0	590	Q4V9V8_MOUSE	Q4V9V8 mus musculus
6	374.5	60.3	614	Q7TMT6_MOUSE	Q7TMT6 mus musculus
7	372.5	60.0	244	Q65ZC8_HUMAN	Q65ZC8 homo sapien
8	372.5	60.0	481	Q91WT1_MOUSE	Q91WT1 mus musculus
9	372	59.9	498	Q6N041_HUMAN	Q6N041 homo sapien
10	369.5	59.5	458	Q5BJZ2_RAT	Q5BJZ2 rattus norv
11	367.5	59.2	125	Q9UL95_HUMAN	Q9UL95 homo sapien
12	366.5	59.0	473	Q9D8L4_MOUSE	Q9D8L4 mus musculus
13	362.5	58.4	480	Q6P089_HUMAN	Q6P089 homo sapien
14	359	57.8	116	Q9UL89_HUMAN	Q9UL89 homo sapien
15	358.5	57.7	146	Q924Q3_MOUSE	Q924Q3 mus musculus
16	358.5	57.7	616	Q504M7_MOUSE	Q504M7 mus musculus
17	358	57.6	518	Q6N030_HUMAN	Q6N030 homo sapien
18	357.5	57.6	125	Q5F2I1_MOUSE	Q5F2I1 mus musculus
19	356.5	57.4	120	Q924Q0_MOUSE	Q924Q0 mus musculus
20	356	57.3	143	Q4KML5_MOUSE	Q4KML5 mus musculus
21	356	57.3	617	Q924Q1_MOUSE	Q924Q1 mus musculus
22	355	57.2	159	Q9GQSO_HUMAN	Q9GQSO homo sapien
23	355	57.2	482	Q8K172_MOUSE	Q8K172 mus musculus
24	354.5	57.1	119	Q9GYZ2_MOUSE	Q9GYZ2 mus musculus
25	354.5	57.1	142	Q924Q1_MOUSE	Q924Q1 mus musculus
26	354.5	57.1	464	Q6PF95_MOUSE	Q6PF95 mus musculus
27	354.5	57.1	483	Q52151_MOUSE	Q52151 mus musculus
28	354	57.0	143	Q924R0_MOUSE	Q924R0 mus musculus
29	353.5	56.9	519	Q5EBM2_HUMAN	Q5EBM2 homo sapien
30	353	56.8	141	Q924Q4_MOUSE	Q924Q4 mus musculus
31	353	56.8	145	Q924R4_MOUSE	Q924R4 mus musculus

32	352.5	56.8	121	1	HV01_MOUSE	P01745 mus musculus
33	352.5	56.8	468	2	Q569W9_MOUSE	Q569W9 mus musculus
34	352	56.7	243	2	Q7TQM2_MOUSE	Q7TQM2 mus musculus
35	351	56.5	469	2	Q7Z7P5_HUMAN	Q7Z7P5 homo sapien
36	351	56.5	475	2	Q6N095_HUMAN	Q6N095 homo sapien
37	350	56.4	136	2	Q7TPE3_MOUSE	Q7TPE3 mus musculus
38	350	56.4	145	2	Q924R1_MOUSE	Q924R1 mus musculus
39	349	56.2	143	2	Q924P9_MOUSE	Q924P9 mus musculus
40	349	56.2	145	2	Q924P7_MOUSE	Q924P7 mus musculus
41	349	56.2	465	2	Q6PJB2_MOUSE	Q6PJB2 mus musculus
42	348.5	56.1	474	2	Q8R3H6_MOUSE	Q8R3H6 mus musculus
43	348.5	56.1	598	2	Q568Y0_RAT	Q568Y0 rattus norv
44	348	56.0	463	2	Q99LC4_MOUSE	Q99LC4 mus musculus
45	347.5	56.0	140	2	Q924R2_MOUSE	Q924R2 mus musculus

ALIGNMENTS

RESULT 1
Q5RE17_PONPY
ID Q5RE17_PONPY PRELIMINARY; PRT; 475 AA.
AC Q5RE17;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Hypothetical protein DKFZp469C2335.
GN Name=DKFZp469C2335;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RG The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR857722; CAH89990.1; -, mRNA.
DR SMR; Q5RE17; 21-475.
DR GO; GO:0030106; P:MHC class I receptor activity; IEA.
DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
DR GO; GO:0019883; P:antigen processing, endogenous antigen via . . ; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG.LIKE; 4.
DR PROSITE; PS00290; IG.MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 51898 MW; 04BBD8096A2CD529 CRC64;

Query Match 69.9%; Score 434; DB 2; Length 475;

Best Local Similarity 68.0%; Pred. No. 2.8e-35;

Matches 85; Conservative 13; Mismatches 17; Indels 10; Gaps 2;

QY 1 EVQLVQSGAEVKKPGESLRISCKGSDSFTTYWGTVQRMQPKGLHWGIIYPGSDITIY 60

DB 20 DIQLVQSGAEVKKPGESLRISCKGSGYFTTYWGTVQRMQPKGLHWGIIYPGSDITIY 79

QY 61 SPFGQGVTTISADKSIISTAYLQWSLKASDTSYVYCTR-----GDRG-----VDYWGQQT 110

DB 80 NRSFEGHITISADMSISTAYLQWTSLKASDSAIYICARLRLSGTNSYHKRSYFQFWGQQT 139

QY 111 LVTVS 115

```
Db 140 LVIVS 144

RESULT 2
Q9UL92_HUMAN
ID Q9UL92_HUMAN PRELIMINARY; PRT; 124 AA.
AC Q9UL92;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA YCung D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035022; AAD56258.1; -; mRNA.
DR HSP; P01751; INQB.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGv; 1_v.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 124
SQ SEQUENCE 124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;

Query Match 62.6%; Score 389; DB 2; Length 124;
Best Local Similarity 59.7%; Pred. No. 2.3e-31;
Matches 74; Conservative 19; Mismatches 23; Indels 8; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDFTTYTWIGVRQMPGKGLWNGIYPGDSITY 60
Db 1 EVQLVESGAEVKKPGASVKASKASGYTFSSYMHVWRQAPQGQLEWNGINPSSGTSY 60
Qy 61 SPSPGQGVTSADKSIISTAYLQWSSLSKASDTAMYCYTRGDRGV-----DYWGQGLTV 112
Db 61 AQKFGKGVTRDTSTSTVYMELSRLSRSDDTAVYVCARGLYVVPAAFRSDYWGQGLTV 120
Qy 113 TVSS 116
Db 121 TVSS 124

RESULT 3
Q9UL94_HUMAN
ID Q9UL94_HUMAN PRELIMINARY; PRT; 119 AA.
AC Q9UL94;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035022; AAD56258.1; -; mRNA.
DR HSP; P01751; INQB.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGv; 1_v.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 124
SQ SEQUENCE 124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;

Query Match 62.6%; Score 389; DB 2; Length 124;
Best Local Similarity 59.7%; Pred. No. 2.3e-31;
Matches 74; Conservative 19; Mismatches 23; Indels 8; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDFTTYTWIGVRQMPGKGLWNGIYPGDSITY 60
Db 1 EVQLVESGAEVKKPGASVKASKASGYTFSSYMHVWRQAPQGQLEWNGINPSSGTSY 60
Qy 61 SPSPGQGVTSADKSIISTAYLQWSSLSKASDTAMYCYTRGDRGV-----DYWGQGLTV 112
Db 61 AQKFGKGVTRDTSTSTVYMELSRLSRSDDTAVYVCARGLYVVPAAFRSDYWGQGLTV 120
Qy 113 TVSS 116
Db 121 TVSS 124

RESULT 3
Q9UL94_HUMAN
ID Q9UL94_HUMAN PRELIMINARY; PRT; 119 AA.
AC Q9UL94;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035022; AAD56258.1; -; mRNA.
DR HSP; P01751; INQB.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGv; 1_v.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 124
SQ SEQUENCE 124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;

Query Match 62.6%; Score 389; DB 2; Length 124;
Best Local Similarity 59.7%; Pred. No. 2.3e-31;
Matches 74; Conservative 19; Mismatches 23; Indels 8; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDFTTYTWIGVRQMPGKGLWNGIYPGDSITY 60
Db 1 EVQLVESGAEVKKPGASVKASKASGYTFSSYMHVWRQAPQGQLEWNGINPSSGTSY 60
Qy 61 SPSPGQGVTSADKSIISTAYLQWSSLSKASDTAMYCYTRGDRGV-----DYWGQGLTV 112
Db 61 AQKFGKGVTRDTSTSTVYMELSRLSRSDDTAVYVCARGLYVVPAAFRSDYWGQGLTV 120
Qy 113 TVSS 116
Db 121 TVSS 124
```

```
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035020; AAD56256.1; -; mRNA.
DR HSP; P01751; INQB.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGv; 1_v.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 119
SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345F4A16E CRC64;

Query Match 61.4%; Score 381.5; DB 2; Length 119;
Best Local Similarity 63.0%; Pred. No. 1.2e-30;
Matches 75; Conservative 18; Mismatches 23; Indels 3; Gaps 2;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDFTTYTWIGVRQMPGKGLWNGIYPGDSITY 60
Db 1 EVQLVESGAEVKKPGASVKASKASGYTFSSYMHVWRQAPQGQLEWNGINPSSWTNY 60
Qy 61 SPSPGQGVTSADKSIISTAYLQWSSLSKASDTAMYCYTRGDRGV-----DYWGQGLTV 116
Db 61 AQKFGKGVTRDTSTSTAYMELSLRSLSDDTAVYVCARGGGRGLWFDPMGQGLTV 119

RESULT 4
Q9Z1C4_MOUSE
ID Q9Z1C4_MOUSE PRELIMINARY; PRT; 118 AA.
AC Q9Z1C4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-porcine VCAM mAb 3F4 heavy chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
STRAIN=Balb/c;
MEDLINE=97450619; PubMed=9307060; DOI=10.1016/S0161-5890(97)00042-4;
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Macis L.A., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT IgG2/G4 constant regions block human leukocyte binding to porcine
RT endothelial cells.";
RL Mol. Immunol. 34:441-452 (1997).
DR EMBL; U78801; AAD00293.1; -; mRNA.
DR HSP; P01751; INQB.
DR SMR; Q9Z1C4; 1-118.
DR Ensembl; ENSMUSG00000021155; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGv; 1_v.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 118
SQ SEQUENCE 118 AA; 13036 MW; 90ECC59D31EC4FC CRC64;

Query Match 61.0%; Score 379; DB 2; Length 118;
Best Local Similarity 57.6%; Pred. No. 2.2e-30;
Matches 68; Conservative 23; Mismatches 25; Indels 2; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDFTTYTWIGVRQMPGKGLWNGIYPGDSITY 60
Db 1 QVQVQSGAEALRPWASVKLSCKASGYNFNSYMQWYKQRFQGLWNGIYPGGDSY 60
Qy 61 SPSPGQGVTSADKSIISTAYLQWSSLSKASDTAMYCYTRGDRG--VDYWGQGLTV 116
Db 61 TQKPRGKATLTADKSSSTAYMQLSLASEDSAVYVCARRTVGGYFDYWGQGLTV 118
```

RESULT 5

Q4V9V8 MOUSE

Q4V9V8 MOUSE PRELIMINARY; PRT; 590 AA.

AC Q4V9V8;

DT 13-SEP-2005 (T-EMBLrel. 31, Created)

DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)

DE Hypothetical protein.

GN Name=Igh-6;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridea; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

[1]

RN NUCLEOTIDE SEQUENCE.

RP

RC TISSUE=Mammary gland;

RX MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Scapleton M., Soares M.B., Bonaldo M.F., Casavet T.L., Scheetz T.E.,

RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,

RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RL mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).

[2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Mammary gland;

RX NIH MGC Project;

RG Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC096667; AAH96667.1; -, mRNA.

DR MGI: MGI:96448; Igh-6

DR InterPro: IPR003599; Ig.

DR InterPro: IPR007110; Ig-like.

DR InterPro: IPR003597; Ig cl.

DR InterPro: IPR003006; Ig MHC.

DR InterPro: IPR003596; Ig v.

DR Pfam: PF07654; Cl-set; 4.

DR SMART: SM00409; IG; 2.

DR SMART: SM00407; IGcl; 4.

DR SMART: SM00406; IGV; 1.

DR PROSITE: PS50835; IG LIKE; 5.

DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.

KW Hypothetical protein.

SQ SEQUENCE 590 AA; 64992 MW; D425318F9A188B14 CRC64;

Query Match 61.0%; Score 379; DB 2; Length 590;

Best Local Similarity 57.8%; Pred. No. 1.3e-29;

Matches 67; Conservative 24; Mismatches 25; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWGVRQMPGKGLGWGIIYPGDSDTIY 60

Db 20 QVQLKQSGAEIIVRPGASVKLSCKASGVTFTDYINWVKRPGQGLEMTARIYPGSGNTY 79

Qy 61 SPSPGQGVTTISADKSIITAYLQWSLKASDPTAMYYCTRGDGVGWGQGLTAVTSS 116

Db 80 NERKPGKATLTAEKSSSTAYMQLSLTSEDSAVYFCARTGTGMDYWGQGTSTVTVSS 135


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DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 498 AA; 54125 MW; 40B3208A84E03B46 CRC64;

Query Match          59.9%; Score 372; DB 2; Length 498;
Best Local Similarity 56.5%; Pred. No. 5.4e-29;
Matches 70; Conservative 20; Mismatches 26; Indels 8; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGWVRQMPGKGLGWGIIYPGDSDTIY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 35 QVQLVQSGADVKKPKGASVKVSKASGYTFITNYFPHWVRQAPQGQPEWGMINPRDGSTKY 94

Qy 61 SPFGQGVTTISADKSIISTAYLQWSSLSKASDTAMYCYTRG-----VDYWGQGTILV 112
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 95 AQRFQGRVSMTRDTSSTIYMELSSLSRSEDAMFFCARAGPGYGTSAYSYFYDYGQGTILV 154

Qy 113 TVSS 116
Db 155 TVSS 158

RESULT 10
Q5BJZ2 RAT PRELIMINARY; PRT; 458 AA.
AC Q5BJZ2;
DT 10-MAY-2005 (TRENBLrel. 30, Created)
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE LOC367586 protein.
GN Name=LOC367586;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
histocompatibility complex class I molecules (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR EMBL; BC091272; AAH91272.1; -; mRNA.
DR SMR; Q5BJZ2; 21-454.

DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG c1.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-sect; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
KW Immunoglobulin domain; Repeat.
SQ SEQUENCE 458 AA; 50161 MW; A0A61DCDD2CA433E CRC64;

Query Match          59.5%; Score 369.5; DB 2; Length 458;
Best Local Similarity 59.0%; Pred. No. 8.8e-29;
Matches 69; Conservative 20; Mismatches 27; Indels 1; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGWVRQMPGKGLGWGIIYPGDSDTIY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLQSQGAELVKPGSSVKISKASGYTFITNYDTHWIKQKQPGNGLEWIIYPGNGTKY 79

Qy 61 SPFGQGVTTISADKSIISTAYLQWSSLSKASDTAMYCYTRG-DRGVVDYWGQGTILVTVSS 116
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NQKNGKATLTADKSSSTAYWQLSSTSDSADVFCARDYDFGVDYWGQGVMTVTVSS 136

RESULT 11
Q5UL95 HUMAN PRELIMINARY; PRT; 125 AA.
AC Q5UL95;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035019; AAD56255.1; -; mRNA.
DR HSSP; P01751; INQB.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON TER
FT NON TER 125
SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;

Query Match          59.2%; Score 367.5; DB 2; Length 125;
Best Local Similarity 56.0%; Pred. No. 3.4e-29;
Matches 70; Conservative 19; Mismatches 27; Indels 9; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGWVRQMPGKGLGWGIIYPGDSDTIY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVESGAELVKPGASVKVSKASGYTFITGYMEHWVRQAPQGQGLEWGMINPSGNTY 60

Qy 61 SPFGQGVTTISADKSIISTAYLQWSSLSKASDTAMYCYTRGDRG-----VDYWGQGTILV 111
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AQKVGQVTVMTDTTISTAYMELSLRSDTAVVYCARSQGGRIAAAGADFDWQGTGM 120

Qy 112 TVTSS 116
Db 121 TVTSS 125
```



```
AC Q6P089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Glandular pool- thyroid;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan E., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prillay S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Glandular pool- thyroid;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC065733; AAH5733.1; -, mRNA.
DR HSSP; P01751; IAGW.
DR SMR; Q6P089; 250-458.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 480 AA; 51997 MW; 2E286C57E4F0BD65 CRC64;

Query Match 58.4%; Score 362.5; DB 2; Length 480;
Best Local Similarity 57.9%; Pred. No. 4.7e-28;
Matches 70; Conservative 19; Mismatches 27; Indels 5; Gaps 1;

QY 1 EVQLVQSGAEVKKPGESLRISCKGSGDFTTYYWGVRQMPGKGLWGMGIYPGSDTIY 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 QVQLVQSGAEVKKTKASVKVSKASGYISDNIHWVRQAPQGLWGMWIRPQNGTIVS 79
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCYTRGDRG-----VDYWGQGLTVTVS 115
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
80 AEKFGQVRVTTITDTSINTAYMELTSLKSDDTALYICARGHSDWSYFYDYGQGLTVTVS 139
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 116 $ 116
Db 140 $ 140
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RESULT 14
Q9UL89 HUMAN PRELIMINARY; PRT; 116 AA.
AC Q9UL89;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1660528;
RA Manheimer-Lofy A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
RA Diamond B.;
RT "Molecular characteristics of antibodies bearing an anti-DNA-
RT associated idiotype.";
RL J. Exp. Med. 174:1639-1652 (1991).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;
RA Hillson J.L., Karr N.S., Opplinger I.R., Mannik M., Sasso E.H.;
RT "The structural basis of germline-encoded VH3 immunoglobulin binding
RT to staphylococcal protein A.";
RL EMBL; AF035025; AAD56261.1; -, mRNA.
DR PIR; PH0870; PH0870.
DR PIR; PH1671; PH1671.
DR HSSP; P01751; INQB.
DR SMR; Q9UL89; 1-115.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12605 MW; C8F9131DE13EA898 CRC64;

Query Match 57.8%; Score 359; DB 2; Length 116;
Best Local Similarity 60.3%; Pred. No. 2.3e-28;
Matches 70; Conservative 17; Mismatches 25; Indels 4; Gaps 1;

QY 5 VQSGAEVKKPGESLRISCKGSGDFTTYYWGVRQMPGKGLWGMGIYPGSDTIYSPSF 64
Db 1 VQSGAEVKKPGSSVKVSKASGTFSSVAISWVRQAPQGLWGMRIIPILGIANYAKF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 65 QGQVTTISADKSIISTAYLQWSSLKASDTAMYCYTRGDRG-----VDYWGQGLTVTVSS 116
Db 61 QGRVTTITADKSTAYMELSLRSEDYAVYYCASNNGPYWYFDLWGRGTLTVTVSS 116
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
Q924Q3 MOUSE PRELIMINARY; PRT; 146 AA.
AC Q924Q3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (fragment).
GN Name=VH186.2-D-J-C mu;
OS Mus musculus (Mouse).
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 14:11:59 ; Search time 31.7224 Seconds
(without alignments)
351.837 Million cell updates/sec

Title: US-10-769-144-4
Perfect score: 621
Sequence: 1 EVQLVQSGAEVKPKPGESLR.....TRGDRGVDMYWGQGLTVTVSS 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	548	88.2	139	2 PH1558	Ig heavy chain V r
2	543.5	87.5	113	2 PH1428	Ig heavy chain V r
3	541.5	87.2	127	2 PH1414	Ig heavy chain V r
4	540.5	87.0	136	2 PH1559	Ig heavy chain V r
5	536.5	86.4	123	2 C36006	Ig heavy chain V r
6	535	86.2	136	2 A49047	Ig heavy chain V r
7	534.5	86.1	123	2 S38492	Ig heavy chain V r
8	529.5	85.3	127	2 PH1415	Ig heavy chain V r
9	525.5	84.6	123	2 PH1413	Ig heavy chain V r
10	525.5	84.6	127	2 PH1411	Ig heavy chain V r
11	524.5	84.5	123	2 PH1423	Ig heavy chain V r
12	520	83.7	134	2 PH1422	Ig heavy chain V r
13	519.5	83.7	117	2 S19670	Ig heavy chain V r
14	519.5	83.7	127	2 PH1420	Ig heavy chain V r
15	513.5	82.7	117	2 S19669	Ig heavy chain V r
16	510	82.1	137	2 PH1562	Ig heavy chain V r
17	508	81.8	126	2 PH1424	Ig heavy chain V r
18	508	81.8	126	2 PH1419	Ig heavy chain V r
19	505	81.3	126	2 PH1416	Ig heavy chain V r
20	504.5	81.2	138	2 PH1565	Ig heavy chain V r
21	502	80.8	126	2 PH1417	Ig heavy chain V r
22	502	80.8	126	2 PH1418	Ig heavy chain V r
23	500	80.5	126	2 PH1412	Ig heavy chain V r
24	499.5	80.4	125	2 PH1410	Ig heavy chain V r
25	496.5	80.0	138	2 PH1564	Ig heavy chain V r
26	496	79.9	122	2 PH1426	Ig heavy chain V r
27	495	79.7	98	2 S26907	Ig heavy chain V r
28	495	79.7	101	2 S12424	Ig heavy chain V r
29	495	79.7	102	2 PH1279	Ig heavy chain V r

RESULT 1

PH1558

Ig heavy chain V region (clone DOB) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 16-Aug-1996

C:Accession: PH1558

R:Rassenti L.Z.; Kipps, T.J.

J. Exp. Med. 177, 1039-1046, 1993

A:Title: Lack of extensive mutations in the VH5 genes used in common B cell chronic lymph

A:Reference number: PH1557; MUID:93210459; PMID:7681468

A:Accession: PH1558

A:Molecule type: DNA

A:Residues: 1-139 <RAS>

A:Cross-references: UNIPARC:UPI0000176581

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:32-115/Domain: immunoglobulin homology <IMM>

Query Match 88.2%; Score 548; DB 2; Length 139;

Best Local Similarity 86.9%; Pred. No. 1.9e-44;

Matches 106; Conservative 2; Mismatches 8; Indels 6; Gaps 1;

Qy 1 EVQLVQSGAEVKPKPGESLRISCKGSGDSFTTYWIGVQRMPGKGLWMGIIYPGSDTRIY 60

Db 18 EVQLVQSGAEVKPKPGESLRISCKGSGYFTSYWIGVQRMPGKGLWMGIIYPGSDTRY 77

Qy 61 SPSPGQQTISADKSISTAYLQWSSLSKASDTAMYYCTRG-----DRGVDYWGQGLTVTV 114

Db 78 SPSPGQQTISADKSISTAYLQWSSLSKASDTAMYYCARSISSSGYISNFDYWGQGLTVTV 137

Qy 115 SS 116

Db 138 SS 139

RESULT 2

PH1428

Ig heavy chain V region (clone VH5-1R1) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 28-May-1999

C:Accession: PH1428

R:van der Stoep, N.; van der Linden, J.; Logtenberg, T.

J. Exp. Med. 177, 99-107, 1993

A:Title: Molecular evolution of the human immunoglobulin E response: High incidence of s

dermatitis.

A:Reference number: PH1409; MUID:93115676; PMID:8418213

A:Accession: PH1428

A:Molecule type: mRNA

A:Residues: 1-113 <VAN>

A:Cross-references: UNIPARC:UPI0000176577; GB:S51905; NID:9262690; PIDN:AAC80261.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin


```
Matches 104; Conservative 4; Mismatches 8; Indels 16; Gaps 1;
Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTWIGWVRQMPGKGLWMMGIIPGSDTIY 60
Db 5 EVQLVQSGAEVKKPGESLRISCKGSGYFTSWIGWVRQMPGKGLWMMGIIPGSDTRY 64
Qy 61 SPSPGQQTISADKSIISTAYLQWSSLKASDTAMYCTRGD-----RGVD 104
Db 65 SPSPGQQTISADKSIISTAYLQWSSLKASDTAMYCARQSYGYDFRSGYTPAYYYGMD 124
Qy 105 YWGQGLTVVSS 116
Db 125 VWGEGTTTVVSS 136

RESULT 7
PHI415
Ig heavy chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
R:Marks, J.D.; Ouweland, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S
submitted to the EMBL Data Library, June 1993
A:Description: Human antibody fragments specific for human blood group antigens from a
A:Reference number: S38488
A:Status: preliminary
A:Accession: S38492
A:Molecule type: DNA
A:Residues: 1-123 <MAN>
A:Cross-references: UNIPARC:UPI000011654D; EMBL:223034; NID:g414031; PIDN:CAA80569.1; PI
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.1%; Score 534.5; DB 2; Length 123;
Best Local Similarity 84.6%; Pred. No. 3.1e-43;
Matches 104; Conservative 4; Mismatches 8; Indels 7; Gaps 1;
Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTWIGWVRQMPGKGLWMMGIIPGSDTIY 60
Db 1 QVQLVQSGAEVKKPGESLRISCKGSGYFTSWIGWVRQMPGKGLWMMGIIPGSDTRY 60
Qy 61 SPSPGQQTISADKSIISTAYLQWSSLKASDTAMYCTR-----GDRGVDYWGQGLTV 113
Db 61 SPSPGQQTISADKSIISTAYLQWSSLKASDTAMYTCARRYSYAQHDWYFDLWGRGTLVT 120
Qy 114 VSS 116
Db 121 VSS 123

RESULT 8
PHI415
Ig heavy chain V region (clone PI-57) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: PHI415
R:van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A:Title: Molecular evolution of the human immunoglobulin E response: High incidence of
dermatitis.
A:Reference number: PHI409; MUID:93115676; PMID:8418213
A:Accession: PHI415
A:Molecule type: mRNA
A:Residues: 1-127 <VAN>
A:Cross-references: UNIPARC:UPI000017694F
A:Experimental source: PBMC
A:Note: the authors translated the codon TTG for residue 118 as Met
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 529.5; DB 2; Length 127;
Best Local Similarity 82.1%; Pred. No. 2.2e-42;
Matches 101; Conservative 6; Mismatches 9; Indels 7; Gaps 1;
```

```
Best Local Similarity 84.6%; Pred. No. 9.3e-43;
Matches 104; Conservative 2; Mismatches 10; Indels 7; Gaps 1;
Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTWIGWVRQMPGKGLWMMGIIPGSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGYFTSWIGWVRQMPGKGLWMMGIIPGSDTRY 60
Qy 61 SPSPGQQTISADKSIISTAYLQWSSLKASDTAMYCTRGD-----RGVDYWGQGLTV 113
Db 61 SPSPGQQTISADKSIISTAYLQWSSLKASDTAMYTCARRDYQDYQSTGTFDPWGQGLTV 120
Qy 114 VSS 116
Db 121 VSS 123

RESULT 9
PHI413
Ig heavy chain V region (clone PI-56) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: PHI413
R:van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A:Title: Molecular evolution of the human immunoglobulin E response: High incidence of
dermatitis.
A:Reference number: PHI409; MUID:93115676; PMID:8418213
A:Accession: PHI413
A:Molecule type: mRNA
A:Residues: 1-123 <VAN>
A:Cross-references: UNIPARC:UPI0000176A34
A:Experimental source: PBMC
A:Note: the authors translated the codon CTG for residue 115 as Met
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 84.6%; Score 525.5; DB 2; Length 123;
Best Local Similarity 84.0%; Pred. No. 2.1e-42;
Matches 100; Conservative 6; Mismatches 10; Indels 3; Gaps 1;
Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTWIGWVRQMPGKGLWMMGIIPGSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGYFTTWIGWVRQMPGKGLWMMGIIPGSDTRY 60
Qy 61 SPSPGQQTISADKSIISTAYLQWSSLKASDTAMYCTRGD---VDYWGQGLTVVSS 116
Db 61 SPSPGQQTISADKSIISTAYLQWSSLKASDTAMYTCARRDDQLMDYWGQGLTVVSS 119

RESULT 10
PHI411
Ig heavy chain V region (clone PI-53) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: PHI411
R:van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A:Title: Molecular evolution of the human immunoglobulin E response: High incidence of
dermatitis.
A:Reference number: PHI409; MUID:93115676; PMID:8418213
A:Accession: PHI411
A:Molecule type: mRNA
A:Residues: 1-127 <VAN>
A:Cross-references: UNIPARC:UPI0000176A32
A:Experimental source: PBMC
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 84.6%; Score 525.5; DB 2; Length 127;
Best Local Similarity 82.1%; Pred. No. 2.2e-42;
Matches 101; Conservative 6; Mismatches 9; Indels 7; Gaps 1;
```


Matches 101; Conservative 6; Mismatches 9; Indels 7; Gaps 2;

Qy 1 EVQLVQSGAEVKPGESLRISCKGSGDSFTTYWGVRQMPKGLGWNGIIPGDSDTIY 60
 Db 1 EVQLVQSGAEVKPGESLRISCKGSGDSFTTYWGVRQMPKGLGWNGIIPGDSDTIY 60

Qy 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYYCTRGDRGV-----DYWGQGLTIVT 113
 Db 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYYCTRGDRGV-----DYWGQGLTIVT 120

Qy 114 VSS 116
 Db 121 VPS 123

RESULT 15

S19669

Ig heavy chain V region (VH5DJ) - human
 C:Species: Homo sapiens (man)
 C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
 C:Accession: S19669
 R:Mark, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
 A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage
 A:Reference number: S19663; MUID:92085276; PMID:1748994
 A:Accession: S19669
 A:Molecule type: mRNA
 A:Residues: 1-117 <MAR>
 A:Cross-references: UNIPARC:UPI0000115FEA; EMBL:X61651; NID:g37731; PIDN:CAA43832.1; PID
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.7%; Score 513.5; DB 2; Length 117;
 Best Local Similarity 83.8%; Pred. NO. 2.7e-41;
 Matches 98; Conservative 7; Mismatches 11; Indels 1; Gaps 1;

Qy 1 EVQLVQSGAEVKPGESLRISCKGSGDSFTTYWGVRQMPKGLGWNGIIPGDSDTIY 60
 Db 1 QVQLVQSGAEVKPGESLRISCKGSGDSFTTYWGVRQMPKGLGWNGIIPGDSDTIY 60

Qy 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYYCTRGDRGV-----DYWGQGLTIVTSS 116
 Db 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYYCTRGDRGV-----DYWGQGLTIVTSS 117

Search completed: December 3, 2005, 14:33:32
 Job time : 32.7225 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 13:27:13 ; Search time 159.086 Seconds
(without alignment)
304.667 Million cell updates/sec

Title: US-10-769-144-4

Perfect score: 621

Sequence: 1 EVQLVQSGAEYKKPGESLR.....TRGDRGVDMYQGQGLTVTVSS 116

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	621	100.0	116	3	US-09-851-614-4	Sequence 4, Appli
2	621	100.0	116	4	US-10-035-637-4	Sequence 4, Appli
3	621	100.0	116	5	US-10-769-144-4	Sequence 4, Appli
4	621	100.0	116	5	US-10-903-191-4	Sequence 4, Appli
5	621	100.0	411	5	US-10-769-144-12	Sequence 12, Appli
6	621	100.0	411	5	US-10-903-191-12	Sequence 12, Appli
7	621	100.0	468	5	US-10-769-144-2	Sequence 2, Appli
8	621	100.0	468	5	US-10-903-191-2	Sequence 2, Appli
9	621	100.0	613	5	US-10-769-144-10	Sequence 10, Appli
10	621	100.0	613	5	US-10-903-191-10	Sequence 10, Appli
11	560	90.2	117	5	US-10-726-332-138	Sequence 138, App
12	558	89.9	117	5	US-10-726-332-9	Sequence 9, Appli
13	556	89.5	120	4	US-10-125-687-6	Sequence 6, Appli
14	556	89.5	120	5	US-10-996-191-6	Sequence 6, Appli
15	552.5	89.0	252	3	US-09-880-748-1537	Sequence 1537, Ap
16	552.5	89.0	252	4	US-10-293-418-1337	Sequence 1337, Ap
17	552	88.9	117	5	US-10-726-332-144	Sequence 144, App
18	550.5	88.6	118	5	US-10-726-332-145	Sequence 145, App
19	550	88.6	224	4	US-10-128-520-167	Sequence 167, App
20	550	88.6	224	4	US-10-128-520-170	Sequence 170, App
21	550	88.6	226	4	US-10-128-520-159	Sequence 159, App
22	548.5	88.3	118	5	US-10-726-332-31	Sequence 31, Appli
23	548.5	88.3	118	5	US-10-726-332-134	Sequence 134, App
24	548.5	88.3	138	4	US-10-395-894-27	Sequence 27, Appli
25	548.5	88.3	138	4	US-10-695-667-27	Sequence 27, Appli
26	548.5	88.3	138	5	US-10-976-352-27	Sequence 27, Appli
27	548	88.2	224	4	US-10-128-520-165	Sequence 165, App

ALIGNMENTS

RESULT 1

US-09-851-614-4
; Sequence 4, Application US/09851614
; Publication No. US20030167502A1
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Keler, Tibor
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: MXI-166
; CURRENT APPLICATION NUMBER: US/09/851,614
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: USSN 60/203,126
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: USSN 60/230,739
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-851-614-4

Query Match 100.0%; Score 621; DB 3; Length 116;
Best Local Similarity 100.0%; Pred. No. 8.2e-49;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEYKKPGESLRISCKGSGDSFTTYWGVRQMPKGLVWGGIYPGSDTIY 60
Db 1 EVQLVQSGAEYKKPGESLRISCKGSGDSFTTYWGVRQMPKGLVWGGIYPGSDTIY 60
Qy 61 SPSPFGQVTTISADKSISTAYLQWSLXKASDTAMTYCTGRGVDMYQGQGLTVTVSS 116
Db 61 SPSPFGQVTTISADKSISTAYLQWSLXKASDTAMTYCTGRGVDMYQGQGLTVTVSS 116

RESULT 2

US-10-035-637-4
; Sequence 4, Application US/10035637
; Publication No. US20030031667A1
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Keler, Tibor
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: MXI-166CP
; CURRENT APPLICATION NUMBER: US/10/035,637
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 09/851,614

Sequence 182, App
Sequence 7, Appli
Sequence 13, Appli
Sequence 29, Appli
Sequence 139, App
Sequence 143, App
Sequence 166, App
Sequence 100, App
Sequence 313, App
Sequence 164, App
Sequence 15, Appli
Sequence 135, App
Sequence 140, App
Sequence 180, App
Sequence 141, App
Sequence 179, App
Sequence 30, Appli
Sequence 162, App

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; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US9N 60/203,126
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: US9N 60/230,739
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-035-637-4

Query Match      100.0%; Score 621; DB 4; Length 116;
Best Local Similarity 100.0%; Pred. No. 8.2e-49;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTYYIWIGVWRQMPGKGLWNGIIPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTYYIWIGVWRQMPGKGLWNGIIPGDSDTIY 60

Qy 61 SPSPGQGVTTISADKSIISTAYLQWSSLSKASDTAMYICTRGDRGVDMGQGLTLVTSS 116
Db 61 SPSPGQGVTTISADKSIISTAYLQWSSLSKASDTAMYICTRGDRGVDMGQGLTLVTSS 116

RESULT 3
US-10-769-144-4
; Sequence 4, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-4

Query Match      100.0%; Score 621; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 8.2e-49;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTYYIWIGVWRQMPGKGLWNGIIPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTYYIWIGVWRQMPGKGLWNGIIPGDSDTIY 60

Qy 61 SPSPGQGVTTISADKSIISTAYLQWSSLSKASDTAMYICTRGDRGVDMGQGLTLVTSS 116
Db 61 SPSPGQGVTTISADKSIISTAYLQWSSLSKASDTAMYICTRGDRGVDMGQGLTLVTSS 116

RESULT 4
US-10-903-191-4
; Sequence 4, Application US/10903191
; Publication No. US20050180983A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
```

```
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301CP
; CURRENT APPLICATION NUMBER: US/10/903,191
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/769144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-903-191-4

Query Match      100.0%; Score 621; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 8.2e-49;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTYYIWIGVWRQMPGKGLWNGIIPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTYYIWIGVWRQMPGKGLWNGIIPGDSDTIY 60

Qy 61 SPSPGQGVTTISADKSIISTAYLQWSSLSKASDTAMYICTRGDRGVDMGQGLTLVTSS 116
Db 61 SPSPGQGVTTISADKSIISTAYLQWSSLSKASDTAMYICTRGDRGVDMGQGLTLVTSS 116

RESULT 5
US-10-769-144-12
; Sequence 12, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-12

Query Match      100.0%; Score 621; DB 5; Length 411;
Best Local Similarity 100.0%; Pred. No. 2.9e-48;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTYYIWIGVWRQMPGKGLWNGIIPGDSDTIY 60
Db 142 EVQLVQSGAEVKKPGESLRISCKGSGDSFTYYIWIGVWRQMPGKGLWNGIIPGDSDTIY 201

Qy 61 SPSPGQGVTTISADKSIISTAYLQWSSLSKASDTAMYICTRGDRGVDMGQGLTLVTSS 116
Db 202 SPSPGQGVTTISADKSIISTAYLQWSSLSKASDTAMYICTRGDRGVDMGQGLTLVTSS 257

RESULT 6
US-10-903-191-12
; Sequence 12, Application US/10903191
; Publication No. US20050180983A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
```

```
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301CP
; CURRENT APPLICATION NUMBER: US/10/903,191
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/769144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-903-191-12

Query Match      100.0%; Score 621; DB 5; Length 411;
Best Local Similarity 100.0%; Pred. No. 2.9e-48;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLWNGIIPGSDTIY 60
Db 142 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLWNGIIPGSDTIY 201

Qy 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVYWGQGLTVTVSS 116
Db 202 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVYWGQGLTVTVSS 257

RESULT 7
US-10-769-144-2
; Sequence 2, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-2

Query Match      100.0%; Score 621; DB 5; Length 468;
Best Local Similarity 100.0%; Pred. No. 3.3e-48;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLWNGIIPGSDTIY 60
Db 20 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLWNGIIPGSDTIY 79

Qy 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVYWGQGLTVTVSS 116
Db 80 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVYWGQGLTVTVSS 135

RESULT 8
US-10-903-191-2
; Sequence 2, Application US/10903191
; Publication No. US20050180983A1
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; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301CP
; CURRENT APPLICATION NUMBER: US/10/903,191
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/769144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-903-191-2

Query Match      100.0%; Score 621; DB 5; Length 468;
Best Local Similarity 100.0%; Pred. No. 3.3e-48;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLWNGIIPGSDTIY 60
Db 20 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLWNGIIPGSDTIY 79

Qy 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVYWGQGLTVTVSS 116
Db 80 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVYWGQGLTVTVSS 135

RESULT 9
US-10-769-144-10
; Sequence 10, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-10

Query Match      100.0%; Score 621; DB 5; Length 613;
Best Local Similarity 100.0%; Pred. No. 4.2e-48;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLWNGIIPGSDTIY 60
Db 20 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLWNGIIPGSDTIY 79

Qy 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVYWGQGLTVTVSS 116
Db 80 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVYWGQGLTVTVSS 135

RESULT 10
```

US-10-903-191-10
; Sequence 10, Application US/10903191
; Publication No. US2005018983A1
; GENERAL INFORMATION:
; APPLICANT: Keller, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ranakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301CP
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: US/10/903,191
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/769144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-903-191-10

Query Match 100.0%; Score 621; DB 5; Length 613;
Best Local Similarity 100.0%; Pred. No. 4.2e-48;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDFTTYIWGVQMPGKGLWNGIYPGDSDTIY 60
Db 20 EVQLVQSGAEVKKPGESLRISCKGSGDFTTYIWGVQMPGKGLWNGIYPGDSDTIY 79
Qy 61 SPSPGQGVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVYWGQGLTVTVSS 116
Db 80 SPSPGQGVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVYWGQGLTVTVSS 135

RESULT 11
US-10-726-332-138
; Sequence 138, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
; FILE REFERENCE: ABGENIX.072A
; CURRENT APPLICATION NUMBER: US/10/726,332
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: n/a
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: 99, 100, 102
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-726-332-138

Query Match 90.2%; Score 560; DB 5; Length 117;
Best Local Similarity 91.4%; Pred. No. 2.9e-43;
Matches 106; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDFTTYIWGVQMPGKGLWNGIYPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDFTTYIWGVQMPGKGLWNGIYPGDSDTIY 60
Qy 61 SPSPGQGVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVYWGQGLTVTVSS 116
Db 61 SPSPGQGVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVYWGQGLTVTVSS 116

RESULT 12
US-10-726-332-9
; Sequence 9, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
; FILE REFERENCE: ABGENIX.072A
; CURRENT APPLICATION NUMBER: US/10/726,332
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: n/a
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-726-332-9

Query Match 89.9%; Score 558; DB 5; Length 117;
Best Local Similarity 91.4%; Pred. No. 4.4e-43;
Matches 106; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDFTTYIWGVQMPGKGLWNGIYPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDFTTYIWGVQMPGKGLWNGIYPGDSDTIY 60
Qy 61 SPSPGQGVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVYWGQGLTVTVSS 116
Db 61 SPSPGQGVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVYWGQGLTVTVSS 116

RESULT 13
US-10-125-687-6
; Sequence 6, Application US/10125687
; Publication No. US20030054407A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; FILE REFERENCE: 26050-705
; CURRENT APPLICATION NUMBER: US/10/125,687
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human consensus antibody heavy chain variable region
US-10-125-687-6

Query Match 89.5%; Score 556; DB 4; Length 120;
Best Local Similarity 89.2%; Pred. No. 6.9e-43;

Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;
 Oy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTWIGWVRQMPKGLKLEWNGIIYPGDSDTIY 60
 Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTWIGWVRQMPKGLKLEWNGIIYPGDSDTIY 60
 Oy 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCTTR-----GDRGVYWGQGLTLVTSS 116
 Db 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCTTR-----GDRGVYWGQGLTLVTSS 120

RESULT 14
 US-10-996-191-6
 ; Sequence 6, Application US/10996191
 ; Publication No. US20050148001A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Luo, Peizhi
 ; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
 ; FILE REFERENCE: 26050-705.301
 ; CURRENT APPLICATION NUMBER: US/10/996,191
 ; CURRENT FILING DATE: 2004-11-22
 ; PRIOR APPLICATION NUMBER: US 60/284,407
 ; PRIOR FILING DATE: 2001-04-17
 ; PRIOR APPLICATION NUMBER: US 10/125,687
 ; PRIOR FILING DATE: 2002-04-17
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 6
 ; LENGTH: 120
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Human consensus antibody heavy chain variable region
 US-10-996-191-6

Query Match 89.5%; Score 556; DB 5; Length 120;
 Best Local Similarity 89.2%; Pred. No. 6.9e-43;
 Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;
 Oy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTWIGWVRQMPKGLKLEWNGIIYPGDSDTIY 60
 Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTWIGWVRQMPKGLKLEWNGIIYPGDSDTIY 60
 Oy 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCTTR-----GDRGVYWGQGLTLVTSS 116
 Db 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCTTR-----GDRGVYWGQGLTLVTSS 120

RESULT 15
 US-09-880-748-1537
 ; Sequence 1537, Application US/09880748
 ; Publication No. US2003005937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
 ; FILE REFERENCE: PF523
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 3239
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1537
 ; LENGTH: 252
 ; TYPE: PRT

; ORGANISM: Homo sapiens
 US-09-880-748-1537
 Query Match 89.0%; Score 552.5; DB 3; Length 252;
 Best Local Similarity 84.8%; Pred. No. 3e-42;
 Matches 106; Conservative 4; Mismatches 9; Gaps 1;
 Oy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTWIGWVRQMPKGLKLEWNGIIYPGDSDTIY 60
 Db 1 QVQLVQSGAEVKKPGESLRISCKGSGDSFTTWIGWVRQMPKGLKLEWNGIIYPGDSDTIY 60
 Oy 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCTTR-----RGVDYWGQGLTL 111
 Db 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCTTR-----RGVDYWGQGLTL 120
 Oy 112 VTVSS 116
 Db 121 VTVSS 125
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 Job time : 160.086 secs

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OM protein - protein search, using sw model

Run on: December 3, 2005, 13:48:29 ; Search time 6.62857 Seconds
(without alignments)
83.796 Million cell updates/sec

Title: US-10-769-144-4

perfect score: 621

PERFECT SCORE: 0.21
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Scoring table: BLOSUM62

scoring table: `BR03sumez`
Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

FOOT-PROCESSING: MINIMUM MATCH 0%
MAXIMUM MATCH 100%

Maximum Match 100%
Listing first 45 summaries

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- | Database : | Table : | Field : | Value : |
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| | | 2 : | /csgn2_6/ptodata1/1/pubpaa/US06_NEW_PUB_pep:* |
| | | 3 : | /csgn2_6/ptodata1/1/pubpaa/US07_NEW_PUB_pep:* |
| | | 4 : | /csgn2_6/ptodata1/1/pubpaa/US08_NEW_PUB_pep:* |
| | | 5 : | /csgn2_6/ptodata1/1/pubpaa/PCT_NEW_PUB_pep:* |
| | | 6 : | /csgn2_6/ptodata1/1/pubpaa/US10_NEW_PUB_pep:* |
| | | 7 : | /csgn2_6/ptodata1/1/pubpaa/US11_NEW_PUB_pep:* |
| | | 8 : | /csgn2_6/ptodata1/1/pubpaa/US60_NEW_PUB_pep:* |

*Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	552.5	89.0	252	7	US-11-054-515-1537	Sequence 1537, Ap	
2	524.5	84.5	249	7	US-11-054-515-1312	Sequence 1312, Ap	
3	501	80.7	248	7	US-11-054-515-2088	Sequence 2088, Ap	
4	498	80.2	248	7	US-11-054-515-1	Sequence 1, Appli	
5	495.5	79.8	248	7	US-11-054-515-1995	Sequence 1995, Ap	
6	495	79.7	98	7	US-11-054-669-45	Sequence 45, Appl	
7	495	79.7	98	7	US-11-084-554-56	Sequence 56, Appl	
8	475.5	76.6	249	7	US-11-054-515-1957	Sequence 1957, Ap	
9	470.5	75.8	247	7	US-11-054-515-2103	Sequence 2103, Ap	
10	447.5	72.1	119	7	US-11-054-515-1204	Sequence 124, App	
11	420.5	67.7	257	7	US-11-054-515-1514	Sequence 1514, Ap	
12	408.5	65.8	125	7	US-11-096-074-58	Sequence 58, Appl	
13	399.5	64.3	121	7	US-11-108-135-24	Sequence 24, Appl	
14	396	63.8	245	7	US-11-054-515-1919	Sequence 1919, Ap	
15	395	63.6	238	7	US-11-054-515-1907	Sequence 1907, Ap	
16	394	63.4	122	7	US-11-105-268-29	Sequence 29, Appl	
17	394	63.4	250	7	US-11-054-515-2097	Sequence 2097, Ap	
18	394	63.4	251	7	US-11-054-515-2001	Sequence 2001, Ap	
19	392	63.1	116	7	US-11-096-074-50	Sequence 50, Appl	
20	392	63.1	246	7	US-11-054-515-2084	Sequence 2084, Ap	
21	392	63.1	251	7	US-11-054-515-1592	Sequence 1592, Ap	
22	391.5	63.0	117	7	US-11-054-669-120	Sequence 120, Appl	
23	390.5	62.9	248	7	US-11-054-515-1104	Sequence 1104, Ap	
24	390	62.8	247	7	US-11-056-825-8	Sequence 8, Appli	
25	390	62.8	248	7	US-11-054-515-1955	Sequence 1955, Ap	

26	390	62.8	24.9	7	US-11-056-925-4	Sequence 4, Appl1
27	389.5	62.7	24.8	7	US-11-054-515-893	Sequence 893, App
28	389.5	62.7	25.1	7	US-11-054-515-930	Sequence 930, App
29	389	62.6	116	7	US-11-174-186-17	Sequence 17, Appl1
30	389	62.6	250	7	US-11-054-515-2093	Sequence 2093, Ap
31	388	62.5	254	7	US-11-054-515-873	Sequence 873, App
32	388	62.5	254	7	US-11-054-515-888	Sequence 888, App
33	388	62.5	254	7	US-11-054-515-1087	Sequence 1087, Ap
34	387	62.3	255	7	US-11-054-515-1156	Sequence 1156, Ap
35	387	62.3	256	7	US-11-054-515-1640	Sequence 1640, Ap
36	386.5	62.2	245	7	US-11-054-515-1946	Sequence 1946, Ap
37	386.5	62.2	248	7	US-11-054-515-2091	Sequence 2091, Ap
38	386.5	62.2	250	7	US-11-054-515-2066	Sequence 2066, Ap
39	385.5	62.1	253	7	US-11-054-515-1813	Sequence 1813, Ap
40	385	62.0	245	7	US-11-054-515-1902	Sequence 1902, Ap
41	385	62.0	253	7	US-11-054-515-1482	Sequence 1482, Ap
42	385	62.0	254	7	US-11-054-515-1088	Sequence 1088, Ap
43	384.5	61.9	248	7	US-11-054-515-1178	Sequence 1178, Ap
44	384.5	61.9	253	7	US-11-054-515-1895	Sequence 1895, Ap
45	384.5	61.9	253	7	US-11-054-515-2098	Sequence 2098, Ap

ALIGNMENTS

```

RESULT 1
US-11-054-515-1537
; Sequence 1537, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2005-02-10
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or P
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1537
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1537

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	Query Match	89.0%; Score 552.5; DB 7;	Length 252;
	Best Local Similarity	84.8%; Pred. No. 8.1e-50;	
	Matches 106; Conservative	4; Mismatches 6;	Gaps 1;
Qy	1 EVQLVQSGAEVKPGESLRISCKGSGSFYYTWIGWRMPGKLEWMGIYPCDSDTIY	60	
	: : : : : :		
Dd	1 QVQLVQSGAEVKPGESLKLICKGSGYSFTSYWIGWRMPGKLEWMGIYPCDSDTRY	60	
	: : : : : :		
Qy	61 SPSPQGQVTISADKSISTAYLQWSSLKASTAMYYCYTRGD-----RGVDYWGGGTLL	111	:

```
Db      61 SPSPQGVTTISADKSI STAYLQWSSLKASDTAMYICARLDYDILTGYPSGFDYWGQTM 120
Qy      112 VTWSS 116
        |||||
Db      121 VTWSS 125

RESULT 2
US-11-054-515-1312
; Sequence 1312, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1312
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1312

Query Match      84.5%; Score 524.5; DB 7; Length 249;
Best Local Similarity 81.6%; Pred. No. 5.6e-47;
Matches 102; Conservative 5; Mismatches 9; Indels 9; Gaps 1;

Qy      1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTYYIGWVRQMPGKGLEWNGIIYPGDSDTIY 60
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 QVQLVQSGAEVKKPGESLRISCKGSGYSFTYIWGVRQMPGKGLEWNGIIPGDSNTRY 60
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      61 SPSPQGVTTISADKSI STAYLQWSSLKASDTAMYICRGRGV-----DYWGQGLT 111
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 SPSPQGVTTISADKSI STAYLQWSSLKASDTAMYICARLYDYDILTGYHWDADFHWGQTM 120
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      112 VTWSS 116
        |||||
Db      121 VTWSS 125

RESULT 3
US-11-054-515-2088
; Sequence 2088, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
```

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; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2088
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2088

Query Match      80.7%; Score 501; DB 7; Length 248;
Best Local Similarity 81.1%; Pred. No. 1.4e-44;
Matches 99; Conservative 4; Mismatches 13; Indels 6; Gaps 1;

Qy      1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTYYIGWVRQMPGKGLEWNGIIPGDSDTIY 60
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 EVQLVQSGAEVKKPGESLRISCKGSGYSFTYIWGVRQMPGKGLEWNGRIDPSDSYTN 60
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      61 SPSPQGVTTISADKSI STAYLQWSSLKASDTAMYICTR-----GDRGVDYWGQGLT 114
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 SPSPQGVTTISADKSI STAYLQWSSLKASDTAIYICARRGTSNYSYSGMDVWGQGLT 120
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      115 SS 116
        ||
Db      121 SS 122

RESULT 4
US-11-054-515-1
; Sequence 1, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
```

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; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1

Query Match      80.2%; Score 498; DB 7; Length 248;
Best Local Similarity 76.2%; Pred. No. 2.7e-44;
Matches 93; Conservative 11; Mismatches 12; Indels 6; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLWNGIIPGDSDTIY 60
Db 1 QVQLQSAALAKPKQSLKISCKSGFTFTTYWIGVWRQLPGKGLWNGIIPGDSHTTY 60

Qy 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGV-----DYWGQGTILTV 114
Db 61 SPSPGHNISVDKSIINTAYLQWSSLKASDTAMYCARHDDDLVLTGYTFESWGQGTMTV 120

Qy 115 SS 116
Db 121 SS 122

RESULT 5
US-11-054-515-1995
; Sequence 1995, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunoespecifically Bind BlyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1995
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1995

Query Match      79.8%; Score 495.5; DB 7; Length 248;
Best Local Similarity 79.7%; Pred. No. 4.9e-44;
Matches 98; Conservative 6; Mismatches 12; Indels 7; Gaps 2;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLWNGIIPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKSGYNFANYIAWVRQTGKGLQGLMGIIYPGDSSTKY 60

Qy 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCTR-GDRGV-----DYWGQGTILTV 113
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Db 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDAMYICARTSERGYROWDFNMGQGTILTV 120
Qy 114 VSS 116
Db 121 VSS 123

RESULT 6
US-11-054-669-45
; Sequence 45, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-45

Query Match      79.7%; Score 495; DB 7; Length 98;
Best Local Similarity 94.9%; Pred. No. 2.1e-44;
Matches 93; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLWNGIIPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKSGYSFTSYWIGVWRQMPGKGLWNGIIPGDSDTY 60

Qy 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCTR 98
Db 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCAR 98

RESULT 7
US-11-084-554-56
; Sequence 56, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-56

Query Match      79.7%; Score 495; DB 7; Length 98;
Best Local Similarity 94.9%; Pred. No. 2.1e-44;
Matches 93; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLWNGIIPGDSDTIY 60
```

Db 1 EVQLVQSGAEVKKPGESLKISCKGSGYFSTYHWLQWVQMPGKGLWNGIIPGDSITRY 60
Qy 61 SPSPQGGVTTISADKSIATYQLWSSLKASDTAMYCYTR 98
Db 61 SPSPQGGVTTISADKSIATYQLWSSLKASDTAMYCYAR 98

RESULT 8

US-11-054-515-1957
; Sequence 1957, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1957
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1957

Query Match 76.6%; Score 475.5; DB 7; Length 249;
Best Local Similarity 76.9%; Pred. No. 5.3e-42;
Matches 93; Conservative 6; Mismatches 17; Indels 5; Gaps 1;
Qy 1 EVQLVQSGAEVKKPGESLKISCKGSGFTTYHWLQWVQMPGKGLWNGIIPGDSITRY 60
Db 1 EVQLVQSGAEVKKPGESLKISCKGYGNYFKGHMIVVQVQPKGLDYNGIIPDSSITY 60
Qy 61 SPSPQGGVTTISADKSIATYQLWSSLKASDTAMYCYC-----TRDGRGVQWQGTTLTVS 115
Db 61 RPSFGQVTTISVDKSTSTAYQLWSSLKASDTAMYCYCARLGLVARGREAFDLWGQGTTLTVS 120
Qy 116 S 116
Db 121 S 121

RESULT 9

US-11-054-515-2103
; Sequence 2103, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10

; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2103
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2103

Query Match 75.8%; Score 470.5; DB 7; Length 247;
Best Local Similarity 76.9%; Pred. No. 1.7e-41;
Matches 93; Conservative 8; Mismatches 15; Indels 5; Gaps 2;
Qy 1 EVQLVQSGAEVKKPGESLKISCKGSGFTTYHWLQWVQMPGKGLWNGIIPGDSITRY 60
Db 1 EVQLVQSGADVKKPGESLKISCKSGYTFANYWITVYVQMPGKGLWNGRIDPSDSYTN 60
Qy 61 SPSPQGGVTTISADKSIATYQLWSSLKASDTAMYCYCTR-----DRGV-DYWGQGTTLTVS 115
Db 61 NPSFGQVTTMSVDKSTNTAYQLWSSLKASDTAKYTCARGGVGDSRGVDFPMGKGTTLTVS 120
Qy 116 S 116
Db 121 S 121

RESULT 10

US-11-054-669-124
; Sequence 124, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 124
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-124

Query Match 72.1%; Score 447.5; DB 7; Length 119;
Best Local Similarity 74.8%; Pred. No. 1.7e-39;
Matches 89; Conservative 6; Mismatches 21; Indels 3; Gaps 1;
Qy 1 EVQLVQSGAEVKKPGESLKISCKGSGFTTYHWLQWVQMPGKGLWNGIIPGDSITRY 60

Db 1 EVQLQSAAEVKKPGESLRISCKTSGYFTSYNHHVVRQMPGKLEWNGAIYPRSGDTSY 60
Qy 61 SPSPQGVTTISADKSIATYLOWSLKASDTAMYCTRG---DRGVYWGQGLTVTVSS 116
Db 61 NPSPQGHVTISADSSSTAYLOWSLKASDAAMYICVRSYDYDAPFAFWGQGLTVTVSS 119

RESULT 11

US-11-054-515-1514
; Sequence 1514, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1514
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1514

Query Match 67.7%; Score 420.5; DB 7; Length 257;
Best Local Similarity 65.1%; Pred. No. 2.1e-36;
Matches 84; Conservative 12; Mismatches 20; Indels 13; Gaps 1;

Qy 1 EVQLVQSAEYVKKPGESLRISCKGSDFTTYWIGWVRQMPGKLEWNGIIPGSDTIY 60
Db 1 EVQLVQSAEYVKKPGESLRISCKGSDFTTYWISWVRQMPGKLEWNGRIDPSYDDY 60
Qy 61 SPSPQGVTTISADKSIATYLOWSLKASDTAMYCTR-----GDRGVYWG 107
Db 61 SPSPKGRVTISDESNAAYLWDSLSQSDATYICARLKAPYDILLTGYPKWFDTWG 120
Qy 108 QGTLTVTVSS 116
Db 121 QGTLTVTVSS 129

RESULT 12

US-11-096-074-58
; Sequence 58, Application US/11096074
; Publication No. US20050260193A1
; GENERAL INFORMATION:
; APPLICANT: LIEBERBURG, IVAN
; TITLE OF INVENTION: STEROID SPARING AGENTS AND METHODS OF USING SAME
; FILE REFERENCE: 034008-112
; CURRENT APPLICATION NUMBER: US/11/096,074
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: 60/558,120

; PRIOR FILING DATE: 2004-04-01
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 58
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-096-074-58

Query Match 65.8%; Score 408.5; DB 7; Length 125;
Best Local Similarity 64.0%; Pred. No. 1.7e-35;
Matches 80; Conservative 16; Mismatches 20; Indels 9; Gaps 2;

Qy 1 EVQLVQSAEYVKKPGESLRISCKGSDFTTYWIGWVRQMPGKLEWNGIIPGSDTIY 60
Db 1 QVQLVQSAEYVKKPGASVKVSKASGYTFTSYAISWVRQAPGQGLEWNGINPGNDITN 60
Qy 61 SPSPQGVTTISADKSIATYLOWSLKASDTAMYCTR-----GDRG-----VDYWGQGL 111
Db 61 AQKFGKRVTTTADTSTSTAYMELSLRSEDATVYICARAPGYSGGCVRYDFYWGQGL 120
Qy 112 VTVSS 116
Db 121 VTVSS 125

RESULT 13

US-11-108-135-24
; Sequence 24, Application US/11108135
; Publication No. US20050260213A1
; GENERAL INFORMATION:
; APPLICANT: Koenig, Scott
; APPLICANT: Veri, Maria Concetta
; APPLICANT: Tuailon, Nadine
; APPLICANT: Bonvini, Ezio
; APPLICANT: Stavenhagen, Jeffrey
; APPLICANT: Rankin, Christopher
; TITLE OF INVENTION: FC-gamma-RIIB-specific antibodies and methods of use thereof
; FILE REFERENCE: 11183-014-999
; CURRENT APPLICATION NUMBER: US/11/108,135
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/562,804
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/582,044
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/582,045
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/654,713
; PRIOR FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Humanized heavy chain variable region
US-11-108-135-24

Query Match 64.3%; Score 399.5; DB 7; Length 121;
Best Local Similarity 62.0%; Pred. No. 1.3e-34;
Matches 75; Conservative 19; Mismatches 22; Indels 5; Gaps 2;

Qy 1 EVQLVQSAEYVKKPGESLRISCKGSDFTTYWIGWVRQMPGKLEWNGIIPGSDTIY 60
Db 1 QVQLVQSAEYVKKPGASVKVSKASGYTFTTYWISWVRQAPGQGLEWNGIDPSITPNY 60
Qy 61 SPSPQGVTTISADKSIATYLOWSLKASDTAMYCTR-GD---RGVDYWGQGLTVTVS 115
Db 61 NKKFGKRVTTTADTSTSTAYMELSLRSDDTAVYICARNGSDSYSGMDYWGQGLTVTVS 120
Qy 116 S 116

```
Db      121 S 121
RESULT 14
US-11-054-515-1919
; Sequence 1919, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1919
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1919

Query Match      63.8%; Score 396; DB 7; Length 245;
Best Local Similarity 61.5%; Pred. No. 6.2e-34;
Matches 75; Conservative 17; Mismatches 24; Indels 6; Gaps 1;

Qy      1 EVQLVQSGAEVKKPGESLRISCKGDSFTTYWGVRQMPGKGLWMMGIIPGDSDTIY 60
Db      1 EVQLVQSGAEVKKPGASVKASKGYFTSYMMHVRQAPGQGLWMMGIINPSSGTSY 60

Qy      61 SPFGQVTTISADKSIATYQLQWSLKSADTAMYYCTRGDGVYWGQGTILTV 114
Db      61 AQKFGRTVMTTRDTSTVTVMELSLRSEDVAVYICARDLSGSYFSRYFDYWGQGTILTV 120

Qy      115 SS 116
Db      121 SS 122

RESULT 15
US-11-054-515-1907
; Sequence 1907, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1919
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1919

Query Match      63.8%; Score 396; DB 7; Length 245;
Best Local Similarity 61.5%; Pred. No. 6.2e-34;
Matches 75; Conservative 17; Mismatches 24; Indels 6; Gaps 1;

Qy      1 EVQLVQSGAEVKKPGESLRISCKGDSFTTYWGVRQMPGKGLWMMGIIPGDSDTIY 60
Db      1 EVQLVQSGAEVKKPGASVKASKGYFTSYMMHVRQAPGQGLWMMGIINPSSGTSY 60

Qy      61 SPFGQVTTISADKSIATYQLQWSLKSADTAMYYCTRGDGVYWGQGTILTV 114
Db      61 AQKFGRTVMTTRDTSTVTVMELSLRSEDVAVYICARDLSGSYFSRYFDYWGQGTILTV 120

Qy      115 SS 116
Db      121 SS 122

; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1907
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1907

Query Match      63.6%; Score 395; DB 7; Length 238;
Best Local Similarity 63.5%; Pred. No. 7.6e-34;
Matches 73; Conservative 18; Mismatches 24; Indels 0; Gaps 0;

Qy      2 VQLVQSGAEVKKPGESLRISCKGDSFTTYWGVRQMPGKGLWMMGIIPGDSDTIYS 61
Db      1 VQLVQSGAEVKKPGASVKASKGYFTTSYGISWVRQAPGQGLWMMGIINPNSGGTNYA 60

Qy      62 PSFGQVTTISADKSIATYQLQWSLKSADTAMYYCTRGDGVYWGQGTILTV 116
Db      61 QKFGRTVMTTRDTSTVTVMELSLRSDDTAVYICARNLWGLDYWGKGTMTVTVSS 115

Search completed: December 3, 2005, 14:17:54
Job time : 7.62857 secs
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